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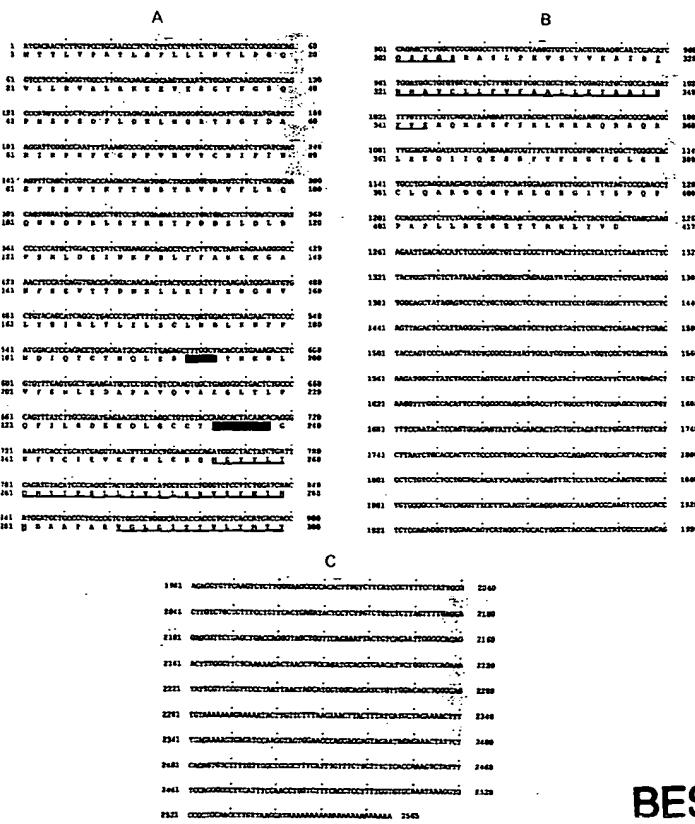
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(54) Title: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT EXPRESSED IN THE GASTROINTESTINAL TRACT, HGRA4, AND SPLICE VARIANT THEREOF



**WO 02/066606 A2**



(57) Abstract: The present invention provides novel polynucleotides encoding HGRA4 polypeptides, fragments and homologues thereof. The present invention also provides novel polynucleotides encoding a HGRA4 splice variant, HGRA4sv. Also provided are vectors, host cells, antibodies, and recombinant and synthetic methods for producing said polypeptides. The invention further relates to diagnostic and therapeutic methods for applying these novel HGRA4 and HGRA4sv polypeptides to the diagnosis, treatment, and/or prevention of various diseases and/or disorders related to these polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of the polynucleotides and polypeptides of the present invention.

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5       **POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR  
ALPHA SUBUNIT EXPRESSED IN THE GASTROINTESTINAL TRACT,  
HGRA4, and SPLICE VARIANT THEREOF**

10       This application claims benefit to provisional application U.S. Serial No.  
10/60/269,535 filed February 16, 2001. The entire teachings of the referenced application  
are incorporated herein by reference.

**FIELD OF THE INVENTION**

15       The present invention provides novel polynucleotides encoding HGRA4  
polypeptides, fragments and homologues thereof. The present invention also provides  
novel polynucleotides encoding a HGRA4 splice variant, HGRA4sv. Also provided  
are vectors, host cells, antibodies, and recombinant and synthetic methods for  
producing said polypeptides. The invention further relates to diagnostic and  
therapeutic methods for applying these novel HGRA4 and HGRA4sv polypeptides to  
20       the diagnosis, treatment, and/or prevention of various diseases and/or disorders related  
to these polypeptides. The invention further relates to screening methods for  
identifying agonists and antagonists of the polynucleotides and polypeptides of the  
present invention.

25

**BACKGROUND OF THE INVENTION**

30       Glycine-mediated inhibitory neurotransmission is essential for voluntary  
motor control, flex responses and sensory signal processing. The receptor for glycine  
is normally found in the spinal cord and the midbrain where it imparts control on  
motor and sensory pathways. The receptor shows selective permeability to the anion  
Cl<sup>-</sup> (Betz, 1991). The receptor is a pentamer of three alpha subunits and two beta  
subunits for a combined molecular weight of approximately 260 kDa. The channel is  
opened to ion flow by the binding of glycine to each of the 3 alpha subunits (Young  
and Snyder, 1974). The glycine receptor is effectively blocked by the compound  
strychnine. To date four different alpha subunits have been cloned and one beta  
35       subunit. Expression of the alpha subunits in oocytes produces a functional receptor  
suggesting that the alpha subunit forms the pore. The beta subunits may have

5 modulatory roles like mediating the fast potentiation of the receptor by calcium (Fucile et al., 2000). An additional subunit, gephyrin, can associate with the intracellular region of the beta-subunit and link the receptor complex to the cytoskeleton via attachment to tubulin (Rajendra et al., 1997). The alpha subunits that have been described are comprised of approximately 420 residues. Hydropathy  
10 analysis predicts an N-terminal extracellular region, four transmembrane domains (TM1-4), and a large intracellular loop between TM3 and TM4. There are two disulfide loops on the extracellular portion of the protein that are essential for receptor function.

Mutations in the glycine receptor alpha 1 gene have been shown cause  
15 hereditary hyperkplexia and spastic paraparesis (Elmslie et al., 1996; Shiang et al., 1993). Studies on antagonists and partial agonists of the glycine receptor have suggested that the glycine receptor has a role in memory deficits in inhibitory avoidance learning (Viu et al., 2000). Other studies have shown that glycine receptors can modulate neurite outgrowth in developing mouse neurons (Tapia et al., 2000).  
20 Recent work in both mouse and hamster sperm have provided evidence for the role of glycine receptors in the acrosome reaction demonstrating that glycine receptors function outside of the nervous system (Llanos et al., 2001; Sato et al., 2000). Agonists and antagonists for these modulating factors could be useful for therapeutic purposes.

25 Using the above examples, it is clear the availability of a novel cloned glycine receptor alpha subunit provides an opportunity for adjunct or replacement therapy, and are useful for the identification of glycine receptor agonists, or stimulators (which might stimulate and/or bias glycine receptor function), as well as, in the identification of glycine receptor inhibitors. All of which might be therapeutically useful under  
30 different circumstances.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells, in addition to their use in the production of HGRA4 polypeptides or HGRA4sv  
35 polypeptides using recombinant techniques. Synthetic methods for producing the polypeptides and polynucleotides of the present invention are provided. Also provided

5 are diagnostic methods for detecting diseases, disorders, and/or conditions related to the HGRA4 and HGRA4sv polypeptides and polynucleotides, and therapeutic methods for treating such diseases, disorders, and/or conditions. The invention further relates to screening methods for identifying binding partners of the polypeptides.

10

## BRIEF SUMMARY OF THE INVENTION

The present invention provides isolated nucleic acid molecules, that comprise, or alternatively consist of, a polynucleotide encoding the HGRA4 protein having the amino acid sequence shown in Figures 1A-C (SEQ ID NO:2) or the amino acid sequence encoded by the cDNA clone, HGRA4 (also referred to as 2BAC10, clone 15 E3, CGR-1, and/or 2BAC10-E3).

The present invention provides isolated nucleic acid molecules, that comprise, or alternatively consist of, a polynucleotide encoding the HGRA4sv protein having the amino acid sequence shown in Figures 2A-B (SEQ ID NO:2) or the amino acid sequence encoded by the cDNA clone, HGRA4sv (also referred to as clone D8, CGR-20 1, and/or 2BAC10-D8) deposited as ATCC Deposit Number PTA-2966 on January 24, 2001. The HGRA4sv polypeptide represents a novel splice variant form of the HGRA4 polypeptide.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing 25 the recombinant vectors, as well as to methods of making such vectors and host cells, in addition to their use in the production of HGRA4 and/or HGRA4sv polypeptides or peptides using recombinant techniques. Synthetic methods for producing the polypeptides and polynucleotides of the present invention are provided. Also provided are diagnostic methods for detecting diseases, disorders, and/or conditions related to 30 the HGRA4 and/or HGRA4sv polypeptides and polynucleotides, and therapeutic methods for treating such diseases, disorders, and/or conditions. The invention further relates to screening methods for identifying binding partners of the polypeptides.

The invention further provides an isolated HGRA4 and/or HGRA4sv polypeptide having an amino acid sequence encoded by a polynucleotide described 35 herein.

5 The invention further relates to a polynucleotide encoding a polypeptide fragment of SEQ ID NO:2, SEQ ID NO:4, or a polypeptide fragment encoded by the cDNA sequence included in the deposited clone, which is hybridizable to SEQ ID NO:1, or SEQ ID NO:3.

10 The invention further relates to a polynucleotide encoding a polypeptide domain of SEQ ID NO:2, SEQ ID NO:4 or a polypeptide domain encoded by the cDNA sequence included in the deposited clone, which is hybridizable to SEQ ID NO:1, or SEQ ID NO:3.

15 The invention further relates to a polynucleotide encoding a polypeptide epitope of SEQ ID NO:2, SEQ ID NO:4 or a polypeptide epitope encoded by the cDNA sequence included in the deposited clone, which is hybridizable to SEQ ID NO:1, or SEQ ID NO:3.

The invention further relates to a polynucleotide encoding a polypeptide of SEQ ID NO:2, SEQ ID NO:4 or the cDNA sequence included in the deposited clone, which is hybridizable to SEQ ID NO:1, or SEQ ID NO:3, having biological activity.

20 The invention further relates to a polynucleotide which is a variant of SEQ ID NO:1, or SEQ ID NO:3.

The invention further relates to a polynucleotide which is an allelic variant of SEQ ID NO:1, or SEQ ID NO:3.

25 The invention further relates to a polynucleotide which encodes a species homologue of the SEQ ID NO:2, SEQ ID NO:4.

The invention further relates to a polynucleotide which represents the complimentary sequence (antisense) of SEQ ID NO:1, or SEQ ID NO:3.

30 The invention further relates to a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified herein, wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

The invention further relates to an isolated nucleic acid molecule of SEQ ID NO:2, SEQ ID NO:4, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a human glycine receptor protein.

35 The invention further relates to an isolated nucleic acid molecule of SEQ ID NO:1, or SEQ ID NO:3, wherein the polynucleotide fragment comprises a nucleotide

5 sequence encoding the sequence identified as SEQ ID NO:2, SEQ ID NO:4 or the polypeptide encoded by the cDNA sequence included in the deposited clone, which is hybridizable to SEQ ID NO:1, or SEQ ID NO:3.

The invention further relates to an isolated nucleic acid molecule of SEQ ID NO:1, or SEQ ID NO:3, wherein the polynucleotide fragment comprises the entire 10 nucleotide sequence of SEQ ID NO:1, or SEQ ID NO:3 or the cDNA sequence included in the deposited clone, which is hybridizable to SEQ ID NO:1, or SEQ ID NO:3.

The invention further relates to an isolated nucleic acid molecule of SEQ ID NO:1, or SEQ ID NO:3, wherein the nucleotide sequence comprises sequential 15 nucleotide deletions from either the C-terminus or the N-terminus.

The invention further relates to an isolated polypeptide comprising an amino acid sequence that comprises a polypeptide fragment of SEQ ID NO:2, SEQ ID NO:4 or the encoded sequence included in the deposited clone.

The invention further relates to a polypeptide fragment of SEQ ID NO:2, SEQ 20 ID NO:4 or the encoded sequence included in the deposited clone, having biological activity.

The invention further relates to a polypeptide domain of SEQ ID NO:2, SEQ ID NO:4 or the encoded sequence included in the deposited clone.

The invention further relates to a polypeptide epitope of SEQ ID NO:2, SEQ 25 ID NO:4 or the encoded sequence included in the deposited clone.

The invention further relates to a full length protein of SEQ ID NO:2, SEQ ID NO:4 or the encoded sequence included in the deposited clone.

The invention further relates to a variant of SEQ ID NO:2, SEQ ID NO:4.

The invention further relates to an allelic variant of SEQ ID NO:2, SEQ 30 ID NO:4. The invention further relates to a species homologue of SEQ ID NO:2, SEQ ID NO:4.

The invention further relates to the isolated polypeptide of SEQ ID NO:2, SEQ ID NO:4, wherein the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

35 The invention further relates to an isolated antibody that binds specifically to the isolated polypeptide of SEQ ID NO:2, SEQ ID NO:4.

5 The invention further relates to a method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of SEQ ID NO:2, SEQ ID NO:4 or the polynucleotide of SEQ ID NO:1, or SEQ ID NO:3.

10 The invention further relates to a method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising the steps of (a) determining the presence or absence of a mutation in the polynucleotide of SEQ ID NO:1, or SEQ ID NO:3; and (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

15 The invention further relates to a method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising the steps of (a) determining the presence or amount of expression of the polypeptide of SEQ ID NO:2, SEQ ID NO:4 in a biological sample; and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or 20 amount of expression of the polypeptide.

The invention further relates to a method for identifying a binding partner to the polypeptide of SEQ ID NO:2, SEQ ID NO:4 comprising the steps of (a) contacting the polypeptide of SEQ ID NO:2, SEQ ID NO:4 with a binding partner; and (b) determining whether the binding partner effects an activity of the polypeptide.

25 The invention further relates to a gene corresponding to the cDNA sequence of SEQ ID NO:1, or SEQ ID NO:3.

The invention further relates to a method of identifying an activity in a biological assay, wherein the method comprises the steps of expressing SEQ ID NO:1, or SEQ ID NO:3 in a cell, (b) isolating the supernatant; (c) detecting an 30 activity in a biological assay; and (d) identifying the protein in the supernatant having the activity.

The invention further relates to a process for making polynucleotide sequences encoding gene products having altered SEQ ID NO:2, SEQ ID NO:4 activity comprising the steps of (a) shuffling a nucleotide sequence of SEQ ID NO:1, or SEQ 35 ID NO:3, (b) expressing the resulting shuffled nucleotide sequences and, (c) selecting

5 for altered activity as compared to the activity of the gene product of said unmodified nucleotide sequence.

The invention further relates to a shuffled polynucleotide sequence produced by a shuffling process, wherein said shuffled DNA molecule encodes a gene product having enhanced tolerance to an inhibitor of SEQ ID NO:2, SEQ ID NO:4 activity.

10 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a cardiovascular disorder

15 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a reproductive disorder.

20 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a neural disorder.

25 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a disorder affecting the peripheral nervous system.

The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a disorder affecting the central nervous system.

30 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a neural disorder related to aberrant excitotoxic cell death.

35 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2,

5 SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a degenerative neural disorder.

The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition 10 is a neural disorder related to chronic peripheral neuropathies

The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a gastrointestinal disorder.

15 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a gastrointestinal disorder related to aberrant longitudinal muscle/myenteric plexus contractions.

20 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a irritable bowel syndrome.

25 The invention further relates to a method for preventing, treating, or ameliorating a medical condition with the polypeptide provided as SEQ ID NO:2, SEQ ID NO:4, in addition to, its encoding nucleic acid, wherein the medical condition is a disorder related to hyper glycine receptor activity.

The invention further relates to a method of identifying a compound that modulates the biological activity of HGRA4 or HGRA4sv, comprising the steps of, 30 (a) combining a candidate modulator compound with HGRA4 or HGRA4sv having the sequence set forth in one or more of SEQ ID NO:2; and measuring an effect of the candidate modulator compound on the activity of HGRA4 or HGRA4sv.

The invention further relates to a method of identifying a compound that modulates the biological activity of a human glycine receptor, comprising the steps of, 35 (a) combining a candidate modulator compound with a host cell expressing HGRA4 or HGRA4sv having the sequence as set forth in SEQ ID NO:2; and , (b) measuring

5 an effect of the candidate modulator compound on the activity of the expressed HGRA4 or HGRA4sv.

The invention further relates to a method of identifying a compound that modulates the biological activity of HGRA4 or HGRA4sv, comprising the steps of, (a) combining a candidate modulator compound with a host cell containing a vector 10 described herein, wherein HGRA4 or HGRA4sv is expressed by the cell; and, (b) measuring an effect of the candidate modulator compound on the activity of the expressed HGRA4 or HGRA4sv.

The invention further relates to a method of screening for a compound that is capable of modulating the biological activity of HGRA4 or HGRA4sv, comprising the 15 steps of: (a) providing a host cell described herein; (b) determining the biological activity of HGRA4 or HGRA4sv in the absence of a modulator compound; (c) contacting the cell with the modulator compound; and (d) determining the biological activity of HGRA4 or HGRA4sv in the presence of the modulator compound; wherein a difference between the activity of HGRA4 or HGRA4sv in the presence of the 20 modulator compound and in the absence of the modulator compound indicates a modulating effect of the compound.

The invention further relates to a compound that modulates the biological activity of human HGRA4 or HGRA4sv as identified by the methods described herein.

25

#### **BRIEF DESCRIPTION OF THE FIGURES/DRAWINGS**

**Figures 1A-C** show the polynucleotide sequence (SEQ ID NO:1) and deduced amino acid sequence (SEQ ID NO:2) of the novel human glycine receptor alpha-subunit, 30 HGRA4, of the present invention. The standard one-letter abbreviation for amino acids is used to illustrate the deduced amino acid sequence. The polynucleotide sequence contains a sequence of 2565 nucleotides (SEQ ID NO:1), encoding a polypeptide of 417 amino acids (SEQ ID NO:2). An analysis of the HGRA4 polypeptide determined that it comprised the following features: three transmembrane 35 domains (TM1 to TM3) located from about amino acid 255 to about amino acid 281 (TM1), from about amino acid 288 to about amino acid 305 (TM2), and/or from about

5 320 to about amino acid 343 (TM3) of SEQ ID NO:2 represented by double underlining; conserved cysteine residues located at amino acid 172, 186, 233, and 244 of SEQ ID NO:2 represented in bold; and conserved ligand binding sites located at about amino acid 193 to about amino acid 195, and from about amino acid 235 to about amino acid 239 of SEQ ID NO:2 represented by shading.

10

**Figures 2A-B** show the polynucleotide sequence (SEQ ID NO: 3) and deduced amino acid sequence (SEQ ID NO:4) of the novel human glycine receptor alpha-subunit splice variant, HGRA4sv, of the present invention. The standard one-letter abbreviation for amino acids is used to illustrate the deduced amino acid sequence.

15 The polynucleotide sequence contains a sequence of 1640 nucleotides (SEQ ID NO:3), encoding a polypeptide of 431 amino acids (SEQ ID NO:4). An analysis of the HGRA4sv polypeptide determined that it comprised the following features: three transmembrane domains (TM1 to TM3) located from about amino acid 269 to about amino acid 295 (TM1), from about amino acid 302 to about amino acid 319 (TM2),  
20 and/or from about 334 to about amino acid 357 (TM3) of SEQ ID NO:4 represented by double underlining; conserved cysteine residues located at amino acid 172, 186, 247, and 258 of SEQ ID NO:4 represented in bold; and conserved ligand binding sites located at about amino acid 208 to about amino acid 209, and from about amino acid 259 to about amino acid 263 of SEQ ID NO:4 represented by shading.

25

**Figures 3A-B** show the regions of similarity between HGRA4 and HGRA4sv to other glycine receptors, specifically, the human glycine receptor alpha-1 subunit protein, also known as, strychnine binding subunit (GRA1; Genbank Accession No. gi|4504019; SEQ ID NO:10); the human glycine receptor alpha 3 subunit protein (GRA3; Genbank Accession No. gi|5729844; SEQ ID NO:11); the mouse glycine receptor subunit alpha 4 protein (GRA4; Genbank Accession No. gi|817957; SEQ ID NO:12); and the human glycine receptor alpha-2 subunit protein (GRA2; Genbank Accession No. gi|4504021; SEQ ID NO:13). The alignment was created using the CLUSTALW algorithm described elsewhere herein using default parameters  
30 (CLUSTALW parameters: gap opening penalty: 10; gap extension penalty: 0.5; gap separation penalty range: 8; percent identity for alignment delay: 40%; and transition  
35 separation penalty range: 8; percent identity for alignment delay: 40%; and transition

5 weighting: 0). The darkly shaded amino acids represent regions of matching identity. The lightly shaded amino acids represent regions of matching similarity. Lines between residues indicate gapped regions for the aligned polypeptides.

10 **Figure 4** shows an expression profile of the novel human glycine receptor alpha subunit, HGRA4. The figure illustrates the relative expression level of HGRA4 amongst various mRNA tissue sources. As shown, transcripts corresponding to HGRA4 expressed predominately in heart tissue. The HGRA4 polypeptide was also expressed significantly in uterus, and to a lesser extent, in testis and spinal cord. Expression data was obtained by measuring the steady state HGRA4 mRNA levels by quantitative PCR using the PCR 15 primer pair provided as SEQ ID NO:7 and 8 as described herein. The expression pattern of the HGRA4 splice variant, HGRA4sv is believed to be the same as for HGRA4.

20 **Figure 5** shows the regions of similarity between HGRA4 and HGRA4sv to the Genescan predicted protein generated from Incyte clone G1934909 (SEQ ID NO:9). The alignment shows the positions of the alternative splice forms of the HGRA4 polypeptide. The residues in bold represent amino acids that are thought to contribute to ligand binding and the formation of disulfide bridges (Rajendra et al., 1997). The alignment was created using the CLUSTALW algorithm described elsewhere herein using default parameters (CLUSTALW parameters: gap opening penalty: 10; gap 25 extension penalty: 0.5; gap separation penalty range: 8; percent identity for alignment delay: 40%; and transition weighting: 0). The amino acids marked with asterisks ("\*") represent regions of matching identity. The lightly shaded amino acids represent regions of matching similarity. Dashes ("—") between residues indicate gapped regions for the aligned polypeptides.

30

**Figure 6** shows a table illustrating the percent identity and percent similarity between the HGRA4 polypeptide of the present invention with the human glycine receptor alpha-1 subunit protein, also known as, strychnine binding subunit (GRA1; Genbank Accession No. gi|4504019; SEQ ID NO:10); the human glycine receptor alpha 3 35 subunit protein (GRA3; Genbank Accession No. gi|5729844; SEQ ID NO:11); the mouse glycine receptor subunit alpha 4 protein (GRA4; Genbank Accession No.

5 gi|817957; SEQ ID NO:12); and the human glycine receptor alpha-2 subunit protein (GRA2; Genbank Accession No. gi|4504021; SEQ ID NO:13). The percent identity and percent similarity values were determined based upon the GAP algorithm (GCG suite of programs; and Henikoff, S. and Henikoff, J. G., Proc. Natl. Acad. Sci. USA 89: 10915-10919(1992)).

10

Figure 7 shows the polynucleotide sequence of an Incyte clone (Incyte Clone No. G1934909). The sequence of this clone corresponds to a portion of the HGRA4 polynucleotides of the present invention. The polynucleotides represented in bold were used in extending the HGRA4 clone sequence to obtain the remaining 15 polynucleotides corresponding to the 5' end of the full-length HGRA4 gene of the present invention.

Figure 8 shows an expression profile of the novel human glycine receptor alpha subunit, HGRA4. The figure illustrates the relative expression level of HGRA4 20 amongst mRNA tissue sources other than those provided in Figure 4 above. As shown, transcripts corresponding to HGRA4 expressed predominately in colon tissue. Expression data was obtained by measuring the steady state HGRA4 mRNA levels by quantitative PCR using the PCR primer pair provided as SEQ ID NO:7 and 8 as described herein. The expression pattern of the HGRA4 splice variant, HGRA4sv is 25 believed to be the same as for HGRA4.

Figure 9 shows an expanded expression profile of the novel human glycine receptor alpha subunit, HGRA4. The figure illustrates the relative expression level of HGPR4 amongst various mRNA tissue sources. As shown, the HGPR4 polypeptide was 30 expressed primarily in the lower gastrointestinal tract (duodenum, jejunum, caecum, colon and rectum), and significantly in the brain, the dorsal root ganglia, the pituitary, ovary and uterus. Expression data was obtained by measuring the steady state HGPR4 mRNA levels by quantitative PCR using the PCR primer pair provided as SEQ ID NO:75 and 76, and Taqman probe (SEQ ID NO:78) as described in Example 5 herein.

35

Table I provides a summary of the novel polypeptides and their encoding polynucleotides of the present invention.

5

**Table II** illustrates the preferred hybridization conditions for the polynucleotides of the present invention. Other hybridization conditions may be known in the art or are described elsewhere herein.

10 **Table III** provides a summary of various conservative substitutions encompassed by the present invention.

#### **DETAILED DESCRIPTION OF THE INVENTION**

15 The present invention may be understood more readily by reference to the following detailed description of the preferred embodiments of the invention and the Examples included herein.

20 The invention provides a novel human sequence that potentially encodes a glycine receptor alpha subunit called HGRA4. The invention also provides a novel splice variant form of the HGRA4 polypeptide, HGRA4sv. Transcripts for HGRA4 are found in the gastrointestinal tissues, to a significant extent in brain, and to a lesser extent, in testis and spinal cord, suggesting that the invention potentially modulates inhibitory neurotransmission function in these tissues. The HGRA4 polynucleotide of the present invention is believed to represent the human ortholog of the partially cloned mouse alpha 4 subunit (Genbank Accession No. gi|817957). Therefore, the 25 polynucleotide of the present invention has been tentatively named HGRA4, for **Human Glycine Receptor Alpha 4**. All references to "HGRA4" shall be construed to apply to HGRA4, and/or HGRA4sv unless otherwise specified herein.

30 In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or 35 mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA

5 preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5 kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:1, SEQ ID NO:3, or the cDNA contained within 20 the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without a signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a 25 molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:1 and SEQ ID NO:3 was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the 30 sequence for SEQ ID NO:3 was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the 35 deposit of microorganisms for purposes of patent procedure. The deposited clone is inserted in the pSport1 plasmid (Life Technologies) using the NotI and Sall restriction

5 endonuclease cleavage sites.

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373, preferably a Model 3700, from Applied Biosystems, Inc.), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

Using the information provided herein, such as the nucleotide sequence in Figures 1A-C (SEQ ID NO:1), a nucleic acid molecule of the present invention encoding the HGRA4 polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning cDNAs using mRNA as starting material. Likewise, a nucleic acid molecule of the present invention encoding the HGRA4sv polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning cDNAs using mRNA as starting material using the information provided herein, such as the nucleotide sequence in Figures 2A-B (SEQ ID NO:3). Illustrative of the invention, the nucleic acid molecule described in Figures 1A-C (SEQ ID NO:1) was discovered in a cDNA library derived from human brain.

35 The determined nucleotide sequence of the HGRA4 cDNA in Figures 1A-C (SEQ ID NO:1) contains an open reading frame encoding a protein of about 417

5 amino acid residues, with a deduced molecular weight of about 47.7 kDa. The amino acid sequence of the predicted HGRA4 polypeptide is shown in Figures 1A-C (SEQ ID NO:2).

10 The determined nucleotide sequence of the HGRA4sv cDNA in Figures 2A-B (SEQ ID NO:3) contains an open reading frame encoding a protein of about 431 amino acid residues, with a deduced molecular weight of about 49 kDa. The amino acid sequence of the predicted HGRA4sv polypeptide is shown in Figures 2A-B (SEQ ID NO:4).

15 A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:1, the complement thereof, to sequences contained in SEQ ID NO:2, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's 20 solution, 10% dextran sulfate, and 20  $\mu$ g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

25 Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH<sub>2</sub>PO<sub>4</sub>; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100  $\mu$ g/ml 30 salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

35 Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include

5 Denhardt's reagent, BLOTT, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

10 Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

15 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of 20 single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA 25 backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

30 The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more 35 detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid

5 side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, 10 and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, 15 cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA 20 mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth 25 Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refer to polynucleotide sequences, while "SEQ ID NO:Y" refer to polypeptide sequences, all four sequences being identified by an integer specified in Table 1 herein.

30 "A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the 35 present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity,

5 and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

The term "organism" as referred to herein is meant to encompass any organism referenced herein, though preferably to eukaryotic organisms, more preferably to mammals, and most preferably to humans.

10 The present invention encompasses the identification of proteins, nucleic acids, or other molecules, that bind to polypeptides and polynucleotides of the present invention (for example, in a receptor-ligand interaction). The polynucleotides of the present invention can also be used in interaction trap assays (such as, for example, that described by Ozenberger and Young (Mol Endocrinol., 9(10):1321-9, (1995); and 15 Ann. N. Y. Acad. Sci., 7;766:279-81, (1995)).

15 The polynucleotide and polypeptides of the present invention are useful as probes for the identification and isolation of full-length cDNAs and/or genomic DNA which correspond to the polynucleotides of the present invention, as probes to hybridize and discover novel, related DNA sequences, as probes for positional 20 cloning of this or a related sequence, as probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides, as probes to quantify gene expression, and as probes for microarrays.

In addition, polynucleotides and polypeptides of the present invention may comprise one, two, three, four, five, six, seven, eight, or more membrane domains.

25 Also, in preferred embodiments the present invention provides methods for further refining the biological function of the polynucleotides and/or polypeptides of the present invention.

30 Specifically, the invention provides methods for using the polynucleotides and polypeptides of the invention to identify orthologs, homologs, paralogs, variants, and/or allelic variants of the invention. Also provided are methods of using the polynucleotides and polypeptides of the invention to identify the entire coding region 35 of the invention, non-coding regions of the invention, regulatory sequences of the invention, and secreted, mature, pro-, prepro-, forms of the invention (as applicable).

In preferred embodiments, the invention provides methods for identifying the 35 glycosylation sites inherent in the polynucleotides and polypeptides of the invention, and the subsequent alteration, deletion, and/or addition of said sites for a number of

5 desirable characteristics which include, but are not limited to, augmentation of protein folding, inhibition of protein aggregation, regulation of intracellular trafficking to organelles, increasing resistance to proteolysis, modulation of protein antigenicity, and mediation of intercellular adhesion.

10 In further preferred embodiments, methods are provided for evolving the polynucleotides and polypeptides of the present invention using molecular evolution techniques in an effort to create and identify novel variants with desired structural, functional, and/or physical characteristics.

15 The present invention further provides for other experimental methods and procedures currently available to derive functional assignments. These procedures include but are not limited to spotting of clones on arrays, micro-array technology, PCR based methods (e.g., quantitative PCR), anti-sense methodology, gene knockout experiments, and other procedures that could use sequence information from clones to build a primer or a hybrid partner.

20 As used herein the terms "modulate" or "modulates" refer to an increase or decrease in the amount, quality or effect of a particular activity, DNA, RNA, or protein.

### Polynucleotides and Polypeptides of the Invention

#### **25 Features of the Polypeptide Encoded by Gene No:1**

30 The polypeptide of this gene provided as SEQ ID NO:2 (Figures 1A-C), encoded by the polynucleotide sequence according to SEQ ID NO:1 (Figures 1A-C), and/or encoded by the polynucleotide contained within the deposited clone, has significant homology at the nucleotide and amino acid level to the human glycine receptor alpha-1 subunit protein, also known as, strychnine binding subunit (GRA1; Genbank Accession No. gi|4504019; SEQ ID NO:10); the human glycine receptor alpha 3 subunit protein (GRA3; Genbank Accession No. gi|5729844; SEQ ID NO:11); the mouse glycine receptor subunit alpha 4 protein (GRA4; Genbank Accession No. gi|817957; SEQ ID NO:12); and the human glycine receptor alpha-2  
35 subunit protein (GRA2; Genbank Accession No. gi|4504021; SEQ ID NO:13). An alignment of the HGRA4 polypeptide with these proteins is provided in Figure 3.

5 The HGRA4 polypeptide was determined to share 90.7% identity and 92.5% similarity with the human glycine receptor alpha-1 subunit protein, also known as, strychnine binding subunit (GRA1; Genbank Accession No. gi|4504019; SEQ ID NO:10); to share 90.7% identity and 92.5% similarity with the human glycine receptor alpha 3 subunit protein (GRA3; Genbank Accession No. gi|5729844; SEQ ID NO:11); to share 90.7% identity and 92.5% similarity with the mouse glycine receptor subunit alpha 4 protein (GRA4; Genbank Accession No. gi|817957; SEQ ID NO:12); and to share 90.7% identity and 92.5% similarity with the human glycine receptor alpha-2 subunit protein (GRA2; Genbank Accession No. gi|4504021; SEQ ID NO:13) as shown in Figure 6.

15 The human glycine receptor alpha-1 subunit protein, also known as, strychnine binding subunit (GRA1; Genbank Accession No. gi|4504019; SEQ ID NO:10) is a human glycine receptor that has been mapped to chromosome 5q32 and found to be linked to the incidence of the autosomal dominant neurologic disorder hereditary hyperekplexia (also known as familial startle disease (STHE)), which is characterized 20 by marked muscle rigidity of central nervous system origin and an exaggerated startle response to unexpected acoustic or tactile stimuli. The incidence of hereditary hyperekplexia was only associated with mutations in exon 6 which resulted in the presence of Arg271 in the mature protein.

25 The human glycine receptor alpha 3 subunit protein (GRA3; Genbank Accession No. gi|5729844; SEQ ID NO:11) is also a human glycine receptor that has been mapped to chromosome 4q33. Two primary splice forms of this protein alpha3L, and alpha3K were identified, in particular, one of the variants (alpha3K) coding. One of the variants lacked the coding sequence for 15 amino acids located within the cytoplasmic loop connecting transmembrane spanning region 3 (TM3) and 30 TM4. Functional expression in HEK 293 cells of alpha3L and alpha3K subunits resulted in the formation of glycine-gated chloride channels that differed significantly in desensitization behavior, thus defining the cytoplasmic loop as an important determinant of channel inactivation kinetics.

35 The HGRA4 polypeptide is believed to represent the human ortholog of the mouse glycine receptor subunit alpha 4 protein based upon its significantly shared percent identity and percent similarity. Based upon the observed homology, the

5 polypeptide of the present invention may share at least some biological activity with glycine receptors, specifically with glycine receptor alpha subunits, more specifically with the mouse glycine receptor subunit alpha 4 protein, in addition to, other glycine receptor alpha subunits referenced elsewhere herein.

10 The HGRA4 polypeptide described herein possesses critical residues that participate in ligand binding, as well as, cysteines that are required for the formation of important disulfide bonds in the extracellular portion of the protein (see Figures 1A-C and 5). Specifically, the ligand binding residues are represented by amino acids from about 193 to about amino acid 195, and from about 235 to about amino acid 239 of SEQ ID NO:2. The conserved cysteine residues are represented by amino acids 15 172, 186, 233, and 244 of SEQ ID NO:2.

20 Most of the known glycine receptors possess four transmembrane domains (TM1 thru TM4). However, analysis of the sequences from multiple clones corresponding to HGRA4 polynucleotides has revealed the presence of a stop codon that truncates the protein by 36 residues, whereby eliminating the last conserved transmembrane domain (TM4) present within other members of the glycine receptor family (see Figures 3A-B). The effect of eliminating this part of the protein is unknown. However, the majority of the sequence that makes up the large cytoplasmic loop between transmembrane domain TM3 and TM4 has been retained. The truncation of the protein in this region should have no effect on the Cl<sup>-</sup> pore (which is 25 comprised of the TM2 domain).

30 The HGRA4 polypeptide has been determined to comprise 3 transmembrane domains (TM1, TM2, and TM3) as shown in Figures 1A-C and 3A-B. The transmembrane domains are located from about amino acid 255 to about amino acid 281 (TM1), from about amino acid 288 to about amino acid 305 (TM2), and/or from about 320 to about amino acid 343 (TM3) of SEQ ID NO:2. In this context, the term “about” may be construed to mean 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids beyond the N-Terminus and/or C-terminus of the above referenced polypeptide.

35 In preferred embodiments, the following transmembrane domain polypeptides are encompassed by the present invention: MGYYLIQMYIPSLLLIVLSWVSWINM (SEQ ID NO:23), VGLGITTVLTMTTQSSGS (SEQ ID NO:24), and/or

5 IWMAVCLLFVFAALLEYAAINFVS (SEQ ID NO:25). Polynucleotides encoding these polypeptides are also provided. The present invention also encompasses the use of the HGRA4 transmembrane polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following N-terminal HGRA4 TM1 transmembrane domain deletion polypeptides are encompassed by the present invention: M1-M27, G2-M27, Y3-M27, Y4-M27, L5-M27, I6-M27, Q7-M27, M8-M27, Y9-M27, I10-M27, P11-M27, S12-M27, L13-M27, L14-M27, I15-M27, V16-M27, I17-M27, L18-M27, S19-M27, W20-M27, and/or V21-M27 of SEQ ID NO:23. Polynucleotide sequences encoding these polypeptides are also provided. The present invention also encompasses the use of these N-terminal HGRA4 TM1 transmembrane domain deletion polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following C-terminal HGRA4 TM1 transmembrane domain deletion polypeptides are encompassed by the present invention: M1-M27, M1-N26, M1-I25, M1-W24, M1-F23, M1-S22, M1-V21, M1-W20, M1-S19, M1-L18, M1-I17, M1-V16, M1-I15, M1-L14, M1-L13, M1-S12, M1-P11, M1-I10, M1-Y9, M1-M8, and/or M1-Q7 of SEQ ID NO:23. Polynucleotide sequences encoding these polypeptides are also provided. The present invention also encompasses the use of these C-terminal HGRA4 TM1 transmembrane domain deletion polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following N-terminal HGRA4 TM2 transmembrane domain deletion polypeptides are encompassed by the present invention: V1-S18, G2-S18, L3-S18, G4-S18, I5-S18, T6-S18, T7-S18, V8-S18, L9-S18, T10-S18, M11-S18, and/or T12-S18 of SEQ ID NO:24. Polynucleotide sequences encoding these polypeptides are also provided. The present invention also encompasses the use of these N-terminal HGRA4 TM2 transmembrane domain deletion polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

35 In preferred embodiments, the following C-terminal HGRA4 TM2 transmembrane domain deletion polypeptides are encompassed by the present

5 invention: V1-S18, V1-G17, V1-S16, V1-S15, V1-Q14, V1-T13, V1-T12, V1-M11,  
V1-T10, V1-L9, V1-V8, and/or V1-T7 of SEQ ID NO:24. Polynucleotide sequences  
encoding these polypeptides are also provided. The present invention also  
encompasses the use of these C-terminal HGRA4 TM2 transmembrane domain  
deletion polypeptides as immunogenic and/or antigenic epitopes as described  
10 elsewhere herein.

In preferred embodiments, the following N-terminal HGRA4 TM3  
transmembrane domain deletion polypeptides are encompassed by the present  
invention: I1-S24, W2-S24, M3-S24, A4-S24, V5-S24, C6-S24, L7-S24, L8-S24, F9-  
15 S24, V10-S24, F11-S24, A12-S24, A13-S24, L14-S24, L15-S24, E16-S24, Y17-S24,  
and/or A18-S24 of SEQ ID NO:25. Polynucleotide sequences encoding these  
polypeptides are also provided. The present invention also encompasses the use of  
these N-terminal HGRA4 TM3 transmembrane domain deletion polypeptides as  
immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following C-terminal HGRA4 TM3  
20 transmembrane domain deletion polypeptides are encompassed by the present  
invention: I1-S24, I1-V23, I1-F22, I1-N21, I1-I20, I1-A19, I1-A18, I1-Y17, I1-E16,  
I1-L15, I1-L14, I1-A13, I1-A12, I1-F11, I1-V10, I1-F9, I1-L8, and/or I1-L7 of SEQ  
ID NO:25. Polynucleotide sequences encoding these polypeptides are also provided.  
The present invention also encompasses the use of these C-terminal HGRA4 TM3  
25 transmembrane domain deletion polypeptides as immunogenic and/or antigenic  
epitopes as described elsewhere herein.

HGRA4 polypeptides and polynucleotides are useful for diagnosing diseases  
related to the over and/or under expression of HGRA4 by identifying mutations in the  
30 HGRA4 gene using HGRA4 sequences as probes or by determining HGRA4 protein  
or mRNA expression levels. HGRA4 polypeptides will be useful in screens for  
compounds that affect the activity of the protein. HGRA4 peptides can also be used  
for the generation of specific antibodies and as bait in yeast two hybrid screens to find  
proteins that specifically interact with HGRA4.

Expression profiling designed to measure the steady state mRNA levels encoding  
35 the HGRA4 polypeptide showed predominately high expression levels in heart and

5 colon; significantly in uterus, and to a lesser extent, in testis and spinal cord (as shown in Figure 4).

Expanded analysis of HGPR4 expression levels by TaqMan™ quantitative PCR (see Figure 9) confirmed that the HGPR4 polypeptide is expressed in the lower gastrointestinal tract (duodenum, jejunum, caecum, colon and rectum). Additional, the 10 HGPR4 was also expressed significantly in the brain, dorsal root ganglia, pituitary, ovary and the uterus. These data suggest that HGPR4 would be useful for treating, detecting, and/or ameliorating disorders or diseases of the central and peripheral nervous system, including various types of syndromes that involve excitotoxic cell death and chronic peripheral neuropathies (neuropathic pain). HGRA4 may also play 15 a role in modulating longitudinal muscle/myenteric plexus contractions, and hence agonists or antagonists of HGRA4 could be used to treat various types of gastrointestinal disorders.

As described elsewhere herein, glycine receptor alpha subunits have been implicated in modulating inhibitory neurotransmission which is essential for 20 voluntary motor control, flex responses and sensory signal processing. Therefore, HGRA4 polynucleotides and polypeptides of the present invention, including agonists and/or fragments thereof, have uses that include, modulating inhibitory neurotransmission which is essential for voluntary motor control, flex responses and sensory signal processing. Moreover, HGRA4 polynucleotides and polypeptides of 25 the present invention, including agonists and/or fragments thereof, have uses that include, but are not limited to modulating neurite outgrowth, modulating the acrosome reaction, and preventing, ameliorating, and treating hyperplexia, spastic paraparesis, and memory deficit in inhibitory learning avoidance.

Depression is related to a decrease in neurotransmitter release. Current 30 treatments of depression include blockers of neurotransmitter uptake, and inhibitors of enzymes involved in neurotransmitter degradation which act to prolong the lifetime of neurotransmitters.

It is believed that certain diseases such as depression, memory disorders and Alzheimer's disease are the result of an impairment in neurotransmitter release.

35 Glycine receptor antagonists may therefore be utilized as cell excitants which may stimulate release of neurotransmitters such as acetylcholine, serotonin and

5 dopamine. Enhanced neurotransmitter release may reverse the symptoms associated with depression and Alzheimer's disease.

The HGRA4 polynucleotides and polypeptides of the present invention, including agonists and/or fragments thereof, have uses that include modulating glycine receptor activity in various cells, tissues, and organisms, and particularly in 10 mammalian brain, heart, colon, uterus, testis, and spinal cord tissue, preferably human. HGRA4 polynucleotides and polypeptides of the present invention, including agonists and/or fragments thereof, may be useful in diagnosing, treating, prognosing, and/or preventing cardiovascular, gastrointestinal, reproductive, and/or neural diseases or disorders.

15 The strong homology to human and mouse glycine receptor alpha subunit proteins, combined with the localized expression in heart suggests HGRA4 polynucleotides and polypeptides of the present invention, including agonists and/or fragments thereof, may be useful in diagnosing, treating, prognosing, and/or preventing cardiovascular diseases and/or disorders, which include, but are not limited 20 to: myocardial infarction, congestive heart failure, arrhythmias, cardiomyopathy, atherosclerosis, arteriosclerosis, microvascular disease, embolism, thrombosis, pulmonary edema, palpitation, dyspnea, angina, hypotension, syncope, heart murmur, aberrant ECG, hypertrophic cardiomyopathy, the Marfan syndrome, sudden death, prolonged QT syndrome, congenital defects, cardiac viral infections, valvular heart 25 disease, hypertension,

Similarly, HGRA4 polynucleotides and polypeptides may be useful for ameliorating cardiovascular diseases and symptoms which result indirectly from various non-cardiovascular effects, which include, but are not limited to, the following, obesity, smoking, Down syndrome (associated with endocardial cushion 30 defect); bony abnormalities of the upper extremities (associated with atrial septal defect in the Holt-Oram syndrome); muscular dystrophies (associated with cardiomyopathy); hemochromatosis and glycogen storage disease (associated with myocardial infiltration and restrictive cardiomyopathy); congenital deafness (associated with prolonged QT interval and serious cardiac arrhythmias); Raynaud's 35 disease (associated with primary pulmonary hypertension and coronary vasospasm); connective tissue disorders, i.e., the Marfan syndrome, Ehlers-Danlos and Hurler

5 syndromes, and related disorders of mucopolysaccharide metabolism (aortic dilatation, prolapsed mitral valve, a variety of arterial abnormalities); acromegaly (hypertension, accelerated coronary atherosclerosis, conduction defects, cardiomyopathy); hyperthyroidism (heart failure, atrial fibrillation); hypothyroidism (pericardial effusion, coronary artery disease); rheumatoid arthritis (pericarditis, aortic 10 valve disease); scleroderma (cor pulmonale, myocardial fibrosis, pericarditis); systemic lupus erythematosus (valvulitis, myocarditis, pericarditis); sarcoidosis (arrhythmias, cardiomyopathy); postmenopausal effects, Chlamydial infections, polycystic ovary disease, thyroid disease, alcoholism, diet, and exfoliative dermatitis (high-output heart failure), for example. Involvement of glycine receptors in 15 cardiovascular function has been previously reported (Kubo, T., Kihara, M, Neurosci, Lett., 74(3):331-6, (1987)).

Moreover, polynucleotides and polypeptides, including fragments and/or antagonists thereof, have uses which include, directly or indirectly, treating, preventing, diagnosing, and/or prognosing the following, non-limiting, cardiovascular 20 infections: blood stream invasion, bacteremia, sepsis, *Streptococcus pneumoniae* infection, group a streptococci infection; group b streptococci infection, *Enterococcus* infection, nonenterococcal group D streptococci infection, nonenterococcal group C streptococci infection, nonenterococcal group G streptococci infection, *Streptoccus viridans* infection, *Staphylococcus aureus* infection, coagulase-negative staphylococci 25 infection, gram-negative Bacilli infection, *Enterobacteriaceae* infection, *Psudomonas* spp. Infection, *Acinobacter* spp. Infection, *Flavobacterium meningosepticum* infection, *Aeromonas* spp. Infection, *Stenotrophomonas maltophilia* infection, gram-negative coccobacilli infection, *Haemophilus influenza* infection, *Branhamella catarrhalis* infection, anaerobe infection, *Bacteroides fragilis* infection, *Clostridium* 30 infection, fungal infection, *Candida* spp. Infection, non-albicans *Candida* spp. Infection, *Hansenula anomala* infection, *Malassezia furfur* infection, nontuberculous *Mycobacteria* infection, *Mycobacterium avium* infection, *Mycobacterium chelonae* infection, *Mycobacterium fortuitum* infection, spirochetal infection, *Borrelia burgdorferi* infection, in addition to any other cardiovascular disease and/or disorder 35 (e.g., non-sepsis) implicated by the causative agents listed above or elsewhere herein.

5        In addition, the strong homology to human and mouse glycine receptor alpha subunit proteins, combined with the localized expression in colon tissue in addition to other gastrointestinal tract tissues, suggests the HGRA4 polynucleotides and polypeptides may be useful in treating, diagnosing, prognosing, and/or preventing gastrointestinal diseases and/or disorders, which include, but are not limited to, ulcers,  
10      irritable bowel syndrome, inflammatory bowel disease, diarrhea, traveler's diarrhea, drug-related diarrhea polyps, absorption disorders, constipation, diverticulitis, vascular disease of the intestines, intestinal obstruction, intestinal infections, ulcerative colitis, Shigellosis, cholera, Crohn's Disease, amebiasis, enteric fever, Whipple's Disease, peritonitis, intrabdominal abscesses, hereditary hemochromatosis,  
15      gastroenteritis, viral gastroenteritis, food poisoning, mesenteric ischemia, mesenteric infarction, in addition to, metabolic diseases and/or disorders.

Moreover, polynucleotides and polypeptides, including fragments and/or antagonists thereof, have uses which include, directly or indirectly, treating, preventing, diagnosing, and/or prognosing susceptibility to the following, non-limiting, gastrointestinal infections: *Salmonella* infection, *E.coli* infection, *E.coli* O157:H7 infection, *Shiga Toxin*-producing *E.coli* infection, *Campylobacter* infection (e.g., *Campylobacter fetus*, *Campylobacter upsaliensis*, *Campylobacter hyoilealis*, *Campylobacter lari*, *Campylobacter jejuni*, *Campylobacter concisus*, *Campylobacter mucosalis*, *Campylobacter sputorum*, *Campylobacter rectus*,  
20      *Campylobacter curvus*, *Campylobacter sputorum*, etc.), *Heliobacter* infection (e.g., *Heliobacter cinaedi*, *Heliobacter fennelliae*, etc.) *Yersinia enterocolitica* infection, *Vibrio* sp. Infection (e.g., *Vibrio mimicus*, *Vibrio parahaemolyticus*, *Vibrio fluvialis*, *Vibrio furnissii*, *Vibrio hollisae*, *Vibrio vulnificus*, *Vibrio alginolyticus*, *Vibrio metschnikovii*, *Vibrio damsela*, *Vibrio cincinnatiensis*, etc.) *Aeromonas* infection  
25      (e.g., *Aeromonas hydrophila*, *Aeromonas sobria*, *Aeromonas caviae*, etc.), *Plesiomonas shigellioides* infection, *Giardia* infection (e.g., *Giardia lamblia*, etc.), *Cryptosporidium* infection, *Listeria* infection, *Entamoeba histolytica* infection, *Rotavirus* infection, *Norwalk* virus infection, *Clostridium difficile* infection, *Clostridium perfringens* infection, *Staphylococcus* infection, *Bacillus* infection, in  
30      addition to any other gastrointestinal disease and/or disorder implicated by the causative agents listed above or elsewhere herein.

5        In addition, antagonists of the HGRA4 polynucleotides and polypeptides may have uses that include diagnosing, treating, prognosing, and/or preventing diseases or disorders related to hyper glycine receptor alpha subunit activity, which may include cardiovascular, gastrointestinal, reproductive, neural, and/or proliferative diseases or disorders.

10      Although it is believed the encoded polypeptide may share at least some biological activities with glycine receptor alpha subunits, a number of methods of determining the exact biological function of this clone are either known in the art or are described elsewhere herein. Briefly, the function of this clone may be determined by applying microarray methodology. Nucleic acids corresponding to the HGRA4 15 polynucleotides, in addition to, other clones of the present invention, may be arrayed on microchips for expression profiling. Depending on which polynucleotide probe is used to hybridize to the slides, a change in expression of a specific gene may provide additional insight into the function of this gene based upon the conditions being studied. For example, an observed increase or decrease in expression levels when the 20 polynucleotide probe used comes from tissue that has been treated with known glycine receptor inhibitors, which include, but are not limited to the drugs listed above, might indicate a function in modulating glycine receptor function, for example. In the case of HGRA4, brain, heart, colon, uterus, testis, and/or spinal cord tissue should be used to extract RNA to prepare the probe.

25      In addition, the function of the protein may be assessed by applying quantitative PCR methodology, for example. Real time quantitative PCR would provide the capability of following the expression of the HGRA4 gene throughout development, for example. Quantitative PCR methodology requires only a nominal amount of tissue from each developmentally important step is needed to perform such 30 experiments. Therefore, the application of quantitative PCR methodology to refining the biological function of this polypeptide is encompassed by the present invention. Also encompassed by the present invention are quantitative PCR probes corresponding to the polynucleotide sequence provided as SEQ ID NO:1 (Figures 1A-C).

35      The function of the protein may also be assessed through complementation assays in yeast. For example, in the case of the HGRA4, transforming yeast deficient

5 in glycine receptor alpha subunit activity and assessing their ability to grow would provide convincing evidence the HGRA4 polypeptide has glycine receptor alpha subunit activity. Additional assay conditions and methods that may be used in assessing the function of the polynucleotides and polypeptides of the present invention are known in the art, some of which are disclosed elsewhere herein.

10 Alternatively, the biological function of the encoded polypeptide may be determined by disrupting a homologue of this polypeptide in Mice and/or rats and observing the resulting phenotype.

Moreover, the biological function of this polypeptide may be determined by the application of antisense and/or sense methodology and the resulting generation of 15 transgenic mice and/or rats. Expressing a particular gene in either sense or antisense orientation in a transgenic mouse or rat could lead to respectively higher or lower expression levels of that particular gene. Altering the endogenous expression levels of a gene can lead to the observation of a particular phenotype that can then be used to derive indications on the function of the gene. The gene can be either over-expressed 20 or under expressed in every cell of the organism at all times using a strong ubiquitous promoter, or it could be expressed in one or more discrete parts of the organism using a well characterized tissue-specific promoter (e.g., a brain, heart, colon, uterus, testis, or spinal cord-specific promoter), or it can be expressed at a specified time of development using an inducible and/or a developmentally regulated promoter.

25 In the case of HGRA4 transgenic mice or rats, if no phenotype is apparent in normal growth conditions, observing the organism under diseased conditions (cardiovascular, gastrointestinal, reproductive, neural, or proliferative disorders, etc.) may lead to understanding the function of the gene. Therefore, the application of antisense and/or sense methodology to the creation of transgenic mice or rats to refine 30 the biological function of the polypeptide is encompassed by the present invention.

In preferred embodiments, the following N-terminal HGRA4 deletion polypeptides are encompassed by the present invention: M1-D417, T2-D417, T3-D417, L4-D417, V5-D417, P6-D417, A7-D417, T8-D417, L9-D417, S10-D417, F11-D417, L12-D417, L13-D417, L14-D417, W15-D417, T16-D417, L17-D417, P18-D417, G19-D417, Q20-D417, V21-D417, L22-D417, L23-D417, R24-D417, V25-D417, A26-D417, L27-D417, A28-D417, K29-D417, E30-D417, E31-D417, V32-

5 D417, K33-D417, S34-D417, G35-D417, T36-D417, K37-D417, G38-D417, S39-  
D417, Q40-D417, P41-D417, M42-D417, S43-D417, P44-D417, S45-D417, D46-  
D417, F47-D417, L48-D417, D49-D417, K50-D417, L51-D417, M52-D417, G53-  
D417, R54-D417, T55-D417, S56-D417, G57-D417, Y58-D417, D59-D417, A60-  
D417, R61-D417, I62-D417, R63-D417, P64-D417, N65-D417, F66-D417, K67-  
10 D417, G68-D417, P69-D417, P70-D417, V71-D417, N72-D417, V73-D417, T74-  
D417, C75-D417, N76-D417, I77-D417, F78-D417, I79-D417, N80-D417, S81-  
D417, F82-D417, S83-D417, S84-D417, V85-D417, T86-D417, K87-D417, T88-  
D417, T89-D417, M90-D417, D91-D417, Y92-D417, R93-D417, V94-D417, N95-  
D417, V96-D417, F97-D417, L98-D417, R99-D417, Q100-D417, Q101-D417,  
15 W102-D417, N103-D417, D104-D417, P105-D417, R106-D417, L107-D417, S108-  
D417, Y109-D417, R110-D417, E111-D417, Y112-D417, P113-D417, D114-D417,  
D115-D417, S116-D417, L117-D417, D118-D417, L119-D417, D120-D417, P121-  
D417, S122-D417, M123-D417, L124-D417, D125-D417, S126-D417, I127-D417,  
W128-D417, K129-D417, P130-D417, D131-D417, L132-D417, F133-D417, F134-  
20 D417, A135-D417, N136-D417, E137-D417, K138-D417, G139-D417, A140-D417,  
N141-D417, F142-D417, H143-D417, E144-D417, V145-D417, T146-D417, T147-  
D417, D148-D417, N149-D417, K150-D417, L151-D417, L152-D417, R153-D417,  
I154-D417, F155-D417, K156-D417, N157-D417, G158-D417, N159-D417, V160-  
D417, L161-D417, Y162-D417, S163-D417, I164-D417, R165-D417, L166-D417,  
25 T167-D417, L168-D417, I169-D417, L170-D417, S171-D417, C172-D417, L173-  
D417, M174-D417, D175-D417, L176-D417, K177-D417, N178-D417, F179-D417,  
P180-D417, M181-D417, D182-D417, I183-D417, Q184-D417, T185-D417, C186-  
D417, T187-D417, M188-D417, Q189-D417, L190-D417, E191-D417, S192-D417,  
F193-D417, G194-D417, Y195-D417, T196-D417, M197-D417, K198-D417, D199-  
30 D417, L200-D417, V201-D417, F202-D417, E203-D417, W204-D417, L205-D417,  
E206-D417, D207-D417, A208-D417, P209-D417, A210-D417, V211-D417, Q212-  
D417, V213-D417, A214-D417, E215-D417, G216-D417, L217-D417, T218-D417,  
L219-D417, P220-D417, Q221-D417, F222-D417, I223-D417, L224-D417, R225-  
D417, D226-D417, E227-D417, K228-D417, D229-D417, L230-D417, G231-D417,  
35 C232-D417, C233-D417, T234-D417, K235-D417, H236-D417, Y237-D417, N238-  
D417, T239-D417, G240-D417, K241-D417, F242-D417, T243-D417, C244-D417,

5 I245-D417, E246-D417, V247-D417, K248-D417, F249-D417, H250-D417, L251-  
D417, E252-D417, R253-D417, Q254-D417, M255-D417, G256-D417, Y257-D417,  
Y258-D417, L259-D417, I260-D417, Q261-D417, M262-D417, Y263-D417, I264-  
D417, P265-D417, S266-D417, L267-D417, L268-D417, I269-D417, V270-D417,  
I271-D417, L272-D417, S273-D417, W274-D417, V275-D417, S276-D417, F277-  
10 D417, W278-D417, I279-D417, N280-D417, M281-D417, D282-D417, A283-D417,  
A284-D417, P285-D417, A286-D417, R287-D417, V288-D417, G289-D417, L290-  
D417, G291-D417, I292-D417, T293-D417, T294-D417, V295-D417, L296-D417,  
T297-D417, M298-D417, T299-D417, T300-D417, Q301-D417, S302-D417, S303-  
D417, G304-D417, S305-D417, R306-D417, A307-D417, S308-D417, L309-D417,  
15 P310-D417, K311-D417, V312-D417, S313-D417, Y314-D417, V315-D417, K316-  
D417, A317-D417, I318-D417, D319-D417, I320-D417, W321-D417, M322-D417,  
A323-D417, V324-D417, C325-D417, L326-D417, L327-D417, F328-D417, V329-  
D417, F330-D417, A331-D417, A332-D417, L333-D417, L334-D417, E335-D417,  
Y336-D417, A337-D417, A338-D417, I339-D417, N340-D417, F341-D417, V342-  
20 D417, S343-D417, R344-D417, Q345-D417, H346-D417, K347-D417, E348-D417,  
F349-D417, I350-D417, R351-D417, L352-D417, R353-D417, R354-D417, R355-  
D417, Q356-D417, R357-D417, R358-D417, Q359-D417, R360-D417, L361-D417,  
E362-D417, E363-D417, D364-D417, I365-D417, I366-D417, Q367-D417, E368-  
D417, S369-D417, R370-D417, F371-D417, Y372-D417, F373-D417, R374-D417,  
25 G375-D417, Y376-D417, G377-D417, L378-D417, G379-D417, H380-D417, C381-  
D417, L382-D417, Q383-D417, A384-D417, R385-D417, D386-D417, G387-D417,  
G388-D417, P389-D417, M390-D417, E391-D417, G392-D417, S393-D417, G394-  
D417, I395-D417, Y396-D417, S397-D417, P398-D417, Q399-D417, P400-D417,  
P401-D417, A402-D417, P403-D417, L404-D417, L405-D417, R406-D417, E407-  
30 D417, G408-D417, E409-D417, T410-D417, and/or T411-D417 of SEQ ID NO:2.  
Polynucleotide sequences encoding these polypeptides are also provided. The present  
invention also encompasses the use of these N-terminal HGRA4 deletion polypeptides  
as immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following C-terminal HGRA4 deletion  
35 polypeptides are encompassed by the present invention: M1-D417, M1-V416, M1-  
Y415, M1-L414, M1-K413, M1-R412, M1-T411, M1-T410, M1-E409, M1-G408,

5 M1-E407, M1-R406, M1-L405, M1-L404, M1-P403, M1-A402, M1-P401, M1-P400,  
M1-Q399, M1-P398, M1-S397, M1-Y396, M1-I395, M1-G394, M1-S393, M1-G392,  
M1-E391, M1-M390, M1-P389, M1-G388, M1-G387, M1-D386, M1-R385, M1-  
A384, M1-Q383, M1-L382, M1-C381, M1-H380, M1-G379, M1-L378, M1-G377,  
M1-Y376, M1-G375, M1-R374, M1-F373, M1-Y372, M1-F371, M1-R370, M1-  
10 S369, M1-E368, M1-Q367, M1-I366, M1-I365, M1-D364, M1-E363, M1-E362, M1-  
L361, M1-R360, M1-Q359, M1-R358, M1-R357, M1-Q356, M1-R355, M1-R354,  
M1-R353, M1-L352, M1-R351, M1-I350, M1-F349, M1-E348, M1-K347, M1-H346,  
M1-Q345, M1-R344, M1-S343, M1-V342, M1-F341, M1-N340, M1-I339, M1-A338,  
M1-A337, M1-Y336, M1-E335, M1-L334, M1-L333, M1-A332, M1-A331, M1-  
15 F330, M1-V329, M1-F328, M1-L327, M1-L326, M1-C325, M1-V324, M1-A323,  
M1-M322, M1-W321, M1-I320, M1-D319, M1-I318, M1-A317, M1-K316, M1-  
V315, M1-Y314, M1-S313, M1-V312, M1-K311, M1-P310, M1-L309, M1-S308,  
M1-A307, M1-R306, M1-S305, M1-G304, M1-S303, M1-S302, M1-Q301, M1-  
20 T300, M1-T299, M1-M298, M1-T297, M1-L296, M1-V295, M1-T294, M1-T293,  
M1-I292, M1-G291, M1-L290, M1-G289, M1-V288, M1-R287, M1-A286, M1-P285,  
M1-A284, M1-A283, M1-D282, M1-M281, M1-N280, M1-I279, M1-W278, M1-  
F277, M1-S276, M1-V275, M1-W274, M1-S273, M1-L272, M1-I271, M1-V270,  
M1-I269, M1-L268, M1-L267, M1-S266, M1-P265, M1-I264, M1-Y263, M1-M262,  
M1-Q261, M1-I260, M1-L259, M1-Y258, M1-Y257, M1-G256, M1-M255, M1-  
25 Q254, M1-R253, M1-E252, M1-L251, M1-H250, M1-F249, M1-K248, M1-V247,  
M1-E246, M1-I245, M1-C244, M1-T243, M1-F242, M1-K241, M1-G240, M1-T239,  
M1-N238, M1-Y237, M1-H236, M1-K235, M1-T234, M1-C233, M1-C232, M1-  
G231, M1-L230, M1-D229, M1-K228, M1-E227, M1-D226, M1-R225, M1-L224,  
M1-I223, M1-F222, M1-Q221, M1-P220, M1-L219, M1-T218, M1-L217, M1-G216,  
30 M1-E215, M1-A214, M1-V213, M1-Q212, M1-V211, M1-A210, M1-P209, M1-  
A208, M1-D207, M1-E206, M1-L205, M1-W204, M1-E203, M1-F202, M1-V201,  
M1-L200, M1-D199, M1-K198, M1-M197, M1-T196, M1-Y195, M1-G194, M1-  
F193, M1-S192, M1-E191, M1-L190, M1-Q189, M1-M188, M1-T187, M1-C186,  
M1-T185, M1-Q184, M1-I183, M1-D182, M1-M181, M1-P180, M1-F179, M1-  
35 N178, M1-K177, M1-L176, M1-D175, M1-M174, M1-L173, M1-C172, M1-S171,  
M1-L170, M1-I169, M1-L168, M1-T167, M1-L166, M1-R165, M1-I164, M1-S163,

5 M1-Y162, M1-L161, M1-V160, M1-N159, M1-G158, M1-N157, M1-K156, M1-F155, M1-I154, M1-R153, M1-L152, M1-L151, M1-K150, M1-N149, M1-D148, M1-T147, M1-T146, M1-V145, M1-E144, M1-H143, M1-F142, M1-N141, M1-A140, M1-G139, M1-K138, M1-E137, M1-N136, M1-A135, M1-F134, M1-F133, M1-L132, M1-D131, M1-P130, M1-K129, M1-W128, M1-I127, M1-S126, M1-  
10 D125, M1-L124, M1-M123, M1-S122, M1-P121, M1-D120, M1-L119, M1-D118, M1-L117, M1-S116, M1-D115, M1-D114, M1-P113, M1-Y112, M1-E111, M1-R110, M1-Y109, M1-S108, M1-L107, M1-R106, M1-P105, M1-D104, M1-N103, M1-W102, M1-Q101, M1-Q100, M1-R99, M1-L98, M1-F97, M1-V96, M1-N95, M1-V94, M1-R93, M1-Y92, M1-D91, M1-M90, M1-T89, M1-T88, M1-K87, M1-  
15 T86, M1-V85, M1-S84, M1-S83, M1-F82, M1-S81, M1-N80, M1-I79, M1-F78, M1-I77, M1-N76, M1-C75, M1-T74, M1-V73, M1-N72, M1-V71, M1-P70, M1-P69, M1-G68, M1-K67, M1-F66, M1-N65, M1-P64, M1-R63, M1-I62, M1-R61, M1-A60, M1-D59, M1-Y58, M1-G57, M1-S56, M1-T55, M1-R54, M1-G53, M1-M52, M1-L51, M1-K50, M1-D49, M1-L48, M1-F47, M1-D46, M1-S45, M1-P44, M1-S43, M1-  
20 M42, M1-P41, M1-Q40, M1-S39, M1-G38, M1-K37, M1-T36, M1-G35, M1-S34, M1-K33, M1-V32, M1-E31, M1-E30, M1-K29, M1-A28, M1-L27, M1-A26, M1-V25, M1-R24, M1-L23, M1-L22, M1-V21, M1-Q20, M1-G19, M1-P18, M1-L17, M1-T16, M1-W15, M1-L14, M1-L13, M1-L12, M1-F11, M1-S10, M1-L9, M1-T8, and/or M1-A7 of SEQ ID NO:2. Polynucleotide sequences encoding these  
25 polypeptides are also provided. The present invention also encompasses the use of these C-terminal HGRA4 deletion polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

Alternatively, preferred polypeptides of the present invention may comprise polypeptide sequences corresponding to, for example, internal regions of the HGRA4 polypeptide (e.g., any combination of both N- and C-terminal HGRA4 polypeptide deletions) of SEQ ID NO:2. For example, internal regions could be defined by the equation: amino acid NX to amino acid CX, wherein NX refers to any N-terminal deletion polypeptide amino acid of HGRA4 (SEQ ID NO:2), and where CX refers to any C-terminal deletion polypeptide amino acid of HGRA4 (SEQ ID NO:2).  
30 Polynucleotides encoding these polypeptides are also provided. The present invention  
35

5 also encompasses the use of these polypeptides as an immunogenic and/or antigenic epitope as described elsewhere herein.

The HGRA4 polypeptide of the present invention was determined to comprise a neurotransmitter gated ion channel domain from about amino acid 44 to about amino acid 341 of SEQ ID NO:2 (Figures 1A-C) according to the Pfam 10 domain analysis algorithm (Bateman, A., Birney, E. R., Durbin, S. R., Eddy, S. R., Howe, K. L., and Sonnhammer, E. L. L., Nucleic Acids Research 28, 263-266 (2000)). In this context, the term "about" should be construed to mean 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 more amino acids in either the N- or C-terminal direction of the above referenced polypeptide. Polynucleotides 15 encoding these polypeptides are also provided.

Neurotransmitter-gated ion channels are transmembrane receptor-ion channel complexes that open transiently upon binding of specific ligands, allowing rapid transmission of signals at chemical synapses.

Of the five families known, four have been shown to form a sequence-related 20 super-family. These are the gamma-aminobutyric acid type A(GABA-A), nicotinic acetylcholine, glycine and the serotonin 5HT3 receptors. The ionotropic glutamate receptors have a distinct primary structure.

However, all these receptors possess a pentameric structure (made up of 25 varying subunits), surrounding a central pore. Each of these subunits contains a large extracellular N-terminal ligand-binding region; 3 hydrophobic transmembrane domains; a large intracellular region; and a fourth hydrophobic domain. Such a domain may also be required for the HGRA4 alpha subunits ability to modulate neurotransmitter transmission.

Preferred polypeptides of the invention comprise the following amino acid 30 sequence:

PSDFLDKLMGRSGYDARIRPNFKGPPVNVCNIFINSFSSVTKTMDYRVNV  
FLRQQWNDPRLSYREYPDDSLDDPSMLDSIWKPDLFFANEKGANFHEVTTD  
NKLLRIFKNGNVLYSIRTLILSCLMDLKNFPMDIQTCTMQLESFGYTMKDLV  
FEWLEDAPAVQVAEGLTPQFILRDEKDLGCCTKHYNTGKFTCIEVKFH  
35 QMGGYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITVLTMTTQSSGSR  
ASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINF (SEQ ID NO:14).

5 Polynucleotides encoding these polypeptides are also provided. The present invention also encompasses the use of this HGRA4 neurotransmitter gated ion channel domain polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

10 The HGRA4 polypeptides of the present invention were determined to comprise several phosphorylation sites based upon the Motif algorithm (Genetics Computer Group, Inc.). The phosphorylation of such sites may regulate some biological activity of the HGRA4 polypeptide. For example, phosphorylation at specific sites may be involved in regulating the protein's ability to associate or bind to other molecules (e.g., proteins, ligands, substrates, DNA, etc.). In the present case, 15 phosphorylation may modulate the ability of the HGRA4 polypeptide to associate with other potassium channel alpha subunits, beta subunits, or its ability to modulate potassium channel function.

20 The HGRA4 polypeptide was predicted to comprise six PKC phosphorylation sites using the Motif algorithm (Genetics Computer Group, Inc.). In vivo, protein kinase C exhibits a preference for the phosphorylation of serine or threonine residues. The PKC phosphorylation sites have the following consensus pattern: [ST]-x-[RK], where S or T represents the site of phosphorylation and 'x' an intervening amino acid residue. Additional information regarding PKC phosphorylation sites can be found in 25 Woodget J.R., Gould K.L., Hunter T., Eur. J. Biochem. 161:177-184(1986), and Kishimoto A., Nishiyama K., Nakanishi H., Uratsuji Y., Nomura H., Takeyama Y., Nishizuka Y., J. Biol. Chem. 260:12492-12499(1985); which are hereby incorporated by reference herein.

30 In preferred embodiments, the following PKC phosphorylation site polypeptides are encompassed by the present invention: NDPRLSYREYPDD (SEQ ID NO:16), GNVLYSIRLTLIL (SEQ ID NO:17), ESFGYTMKDLVFE (SEQ ID NO:18), TKHYNTGKFTCIE (SEQ ID NO:19), LREGETTRKLYVD (SEQ ID NO:20), and/or REGETTRKLYVD (SEQ ID NO:21). Polynucleotides encoding these polypeptides are also provided.

35 The present invention also encompasses immunogenic and/or antigenic epitopes of the HGRA4 polypeptide.

5. The HGRA4 polypeptide has been shown to comprise one glycosylation site according to the Motif algorithm (Genetics Computer Group, Inc.). As discussed more specifically herein, protein glycosylation is thought to serve a variety of functions including: augmentation of protein folding, inhibition of protein aggregation, regulation of intracellular trafficking to organelles, increasing resistance to 10 proteolysis, modulation of protein antigenicity, and mediation of intercellular adhesion.

Asparagine phosphorylation sites have the following consensus pattern, N-{P}-[ST]-{P}, wherein N represents the glycosylation site. However, it is well known that that potential N-glycosylation sites are specific to the consensus sequence Asn- 15 Xaa-Ser/Thr. However, the presence of the consensus tripeptide is not sufficient to conclude that an asparagine residue is glycosylated, due to the fact that the folding of the protein plays an important role in the regulation of N-glycosylation. It has been shown that the presence of proline between Asn and Ser/Thr will inhibit N-glycosylation; this has been confirmed by a recent statistical analysis of glycosylation 20 sites, which also shows that about 50% of the sites that have a proline C-terminal to Ser/Thr are not glycosylated. Additional information relating to asparagine glycosylation may be found in reference to the following publications, which are hereby incorporated by reference herein: Marshall R.D., Annu. Rev. Biochem. 41:673-702(1972); Pless D.D., Lennarz W.J., Proc. Natl. Acad. Sci. U.S.A. 74:134- 25 138(1977); Bause E., Biochem. J. 209:331-336(1983); Gavel Y., von Heijne G., Protein Eng. 3:433-442(1990); and Miletich J.P., Broze G.J. Jr., J. Biol. Chem.. 265:11397-11404(1990).

In preferred embodiments, the following asparagine glycosylation site 30 polypeptides are encompassed by the present invention: KGPPVNVTNCNIFIN (SEQ ID NO:22). Polynucleotides encoding these polypeptides are also provided. The present invention also encompasses the use of these HGRA4 asparagine glycosylation site polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

Many polynucleotide sequences, such as EST sequences, are publicly 35 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO: 1 and may have been publicly available prior to conception of

5 the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides consisting of a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2551 of SEQ ID NO:1, b  
10 is an integer between 15 to 2565, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:1, and where b is greater than or equal to a+14.

#### **Features of the Polypeptide Encoded by Gene No:2**

15 The polypeptide of this gene provided as SEQ ID NO:4 (Figures 2A-B), encoded by the polynucleotide sequence according to SEQ ID NO:3 (Figures 2A-B), and/or encoded by the polynucleotide contained within the deposited clone, HGPR4, has significant homology at the nucleotide and amino acid level to the human glycine receptor alpha-1 subunit protein, also known as, strychnine binding subunit (GRA1);  
20 Genbank Accession No. gi|4504019; SEQ ID NO:30); the human glycine receptor alpha 3 subunit protein (GRA3; Genbank Accession No. gi|5729844; SEQ ID NO:31); the mouse glycine receptor subunit alpha 4 protein (GRA4; Genbank Accession No. gi|817957; SEQ ID NO:32); and the human glycine receptor alpha-2 subunit protein (GRA2; Genbank Accession No. gi|4504021; SEQ ID NO:33). An  
25 alignment of the HGRA4sv polypeptide with these proteins is provided in Figure 3.

The HGRA4sv polypeptide was determined to share 76.8% identity and 82.2% similarity with the human glycine receptor alpha-1 subunit protein, also known as, strychnine binding subunit (GRA1; Genbank Accession No. gi|4504019; SEQ ID NO:30); to share 84.4% identity and 78.7% similarity with the human glycine receptor alpha 3 subunit protein (GRA3; Genbank Accession No. gi|5729844; SEQ ID NO:31); to share 97% identity and 96% similarity with the mouse glycine receptor subunit alpha 4 protein (GRA4; Genbank Accession No. gi|817957; SEQ ID NO:32); and to share 80.6% identity and 86.5% similarity with the human glycine receptor alpha-2 subunit protein (GRA2; Genbank Accession No. gi|4504021; SEQ ID NO:33)  
35 as shown in Figure 6.

5        The human glycine receptor alpha-1 subunit protein, also known as, strychnine binding subunit (GRA1; Genbank Accession No. gi|4504019; SEQ ID NO:10) is a human glycine receptor that has been mapped to chromosome 5q32 and found to be linked to the incidence of the autosomal dominant neurologic disorder hereditary hyperekplexia (also known as familial startle disease (STHE)), which is characterized  
10      by marked muscle rigidity of central nervous system origin and an exaggerated startle response to unexpected acoustic or tactile stimuli. The incidence of hereditary hyperekplexia was only associated with mutations in exon 6 which resulted in the presence of Arg271 in the mature protein.

15      The human glycine receptor alpha 3 subunit protein (GRA3; Genbank Accession No. gi|5729844; SEQ ID NO:11) is also a human glycine receptor that has been mapped to chromosome 4q33. Two primary splice forms of this protein alpha3L, and alpha3K were identified, in particular, one of the variants (alpha3K) coding. One of the variants lacked the coding sequence for 15 amino acids located within the cytoplasmic loop connecting transmembrane spanning region 3 (TM3) and  
20      TM4. Functional expression in HEK 293 cells of alpha3L and alpha3K subunits resulted in the formation of glycine-gated chloride channels that differed significantly in desensitization behavior, thus defining the cytoplasmic loop as an important determinant of channel inactivation kinetics.

25      The HGRA4sv polypeptide is believed to represent the a novel splice variant of the human ortholog of the mouse glycine receptor subunit alpha 4 protein based upon its significantly shared percent identity and percent similarity. Based upon the observed homology, the polypeptide of the present invention may share at least some biological activity with glycine receptors, specifically with glycine receptor alpha subunits, more specifically with the mouse glycine receptor subunit alpha 4 protein, in  
30      addition to, other glycine receptor alpha subunits referenced elsewhere herein.

35      The HGRA4sv polypeptide described herein possesses critical residues that participate in ligand binding, as well as, cysteines that are required for the formation of important disulfide bonds in the extracellular portion of the protein (see Figures 2A-B and 5). Specifically, the ligand binding residues are represented by amino acids from about 208 to about amino acid 209, and from about 259 to about amino acid 263

5 of SEQ ID NO:4. The conserved cysteine residues are represented by amino acids 172, 186, 247, and 258 of SEQ ID NO:4.

The present invention also encompasses the HGRA4sv splice variant peptide fragment represented by amino acids from about 191 to about amino acid 207 of SEQ ID NO:4.

10 In preferred embodiments, the following HGRA4sv splice variant peptide fragment polypeptide is encompassed by the present invention: SSSILCSPPLPSLSSLV (SEQ ID NO:74). Polynucleotides encoding this polypeptide are also provided. The present invention also encompasses the use of the HGRA4sv splice variant peptide fragment polypeptide as an immunogenic and/or antigenic 15 epitope as described elsewhere herein.

Most of the known glycine receptors possess four transmembrane domains (TM1 thru TM4). However, analysis of the sequences from multiple clones corresponding to HGRA4sv polynucleotides has revealed the presence of a stop codon that truncates the protein by 36 residues, whereby eliminating the last 20 conserved transmembrane domain (TM4) present within other members of the glycine receptor family (see Figures 3A-B). The effect of eliminating this part of the protein is unknown. However, the majority of the sequence that makes up the large cytoplasmic loop between transmembrane domain TM3 and TM4 has been retained. The truncation of the protein in this region should have no effect on the Cl- pore (which is 25 comprised of the TM2 domain).

The HGRA4sv polypeptide has been determined to comprise 3 transmembrane domains (TM1, TM2, and TM3) as shown in Figures 2A-B and 3A-B. The transmembrane domains are located from about amino acid 269 to about amino acid 295 (TM1), from about amino acid 302 to about amino acid 319 (TM2), and/or from 30 about 334 to about amino acid 357 (TM3) of SEQ ID NO:4. In this context, the term "about" may be construed to mean 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids beyond the N-Terminus and/or C-terminus of the above referenced polypeptide.

In preferred embodiments, the following transmembrane domain polypeptides are encompassed by the present invention: MGYYLIQMYIPSLLLIVILSWVSWINM 35 (SEQ ID NO:26), VGLGITTVLMTTQSSGS (SEQ ID NO:27), and/or

5 IWMAVCLLFVFAALLEYAAINFVS (SEQ ID NO:28). Polynucleotides encoding these polypeptides are also provided. The present invention also encompasses the use of the HGRA4sv transmembrane polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following N-terminal HGRA4sv TM1 transmembrane domain deletion polypeptides are encompassed by the present invention: M1-M27, G2-M27, Y3-M27, Y4-M27, L5-M27, I6-M27, Q7-M27, M8-M27, Y9-M27, I10-M27, P11-M27, S12-M27, L13-M27, L14-M27, I15-M27, V16-M27, I17-M27, L18-M27, S19-M27, W20-M27, and/or V21-M27 of SEQ ID NO:26. Polynucleotide sequences encoding these polypeptides are also provided. The present invention also encompasses the use of these N-terminal HGRA4sv TM1 transmembrane domain deletion polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following C-terminal HGRA4sv TM1 transmembrane domain deletion polypeptides are encompassed by the present invention: M1-M27, M1-N26, M1-I25, M1-W24, M1-F23, M1-S22, M1-V21, M1-W20, M1-S19, M1-L18, M1-I17, M1-V16, M1-I15, M1-L14, M1-L13, M1-S12, M1-P11, M1-I10, M1-Y9, M1-M8, and/or M1-Q7 of SEQ ID NO:26. Polynucleotide sequences encoding these polypeptides are also provided. The present invention also encompasses the use of these C-terminal HGRA4sv TM1 transmembrane domain deletion polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following N-terminal HGRA4sv TM2 transmembrane domain deletion polypeptides are encompassed by the present invention: V1-S18, G2-S18, L3-S18, G4-S18, I5-S18, T6-S18, T7-S18, V8-S18, L9-S18, T10-S18, M11-S18, and/or T12-S18 of SEQ ID NO:27. Polynucleotide sequences encoding these polypeptides are also provided. The present invention also encompasses the use of these N-terminal HGRA4sv TM2 transmembrane domain deletion polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

35 In preferred embodiments, the following C-terminal HGRA4sv TM2 transmembrane domain deletion polypeptides are encompassed by the present

5 invention: V1-S18, V1-G17, V1-S16, V1-S15, V1-Q14, V1-T13, V1-T12, V1-M11,  
10 V1-T10, V1-L9, V1-V8, and/or V1-T7 of SEQ ID NO:27. Polynucleotide sequences  
encoding these polypeptides are also provided. The present invention also  
encompasses the use of these C-terminal HGRA4sv TM2 transmembrane domain  
deletion polypeptides as immunogenic and/or antigenic epitopes as described  
10 elsewhere herein.

In preferred embodiments, the following N-terminal HGRA4sv TM3  
transmembrane domain deletion polypeptides are encompassed by the present  
invention: I1-S24, W2-S24, M3-S24, A4-S24, V5-S24, C6-S24, L7-S24, L8-S24, F9-  
15 S24, V10-S24, F11-S24, A12-S24, A13-S24, L14-S24, L15-S24, E16-S24, Y17-S24,  
and/or A18-S24 of SEQ ID NO:28. Polynucleotide sequences encoding these  
polypeptides are also provided. The present invention also encompasses the use of  
these N-terminal HGRA4sv TM3 transmembrane domain deletion polypeptides as  
immunogenic and/or antigenic epitopes as described elsewhere herein.

In preferred embodiments, the following C-terminal HGRA4sv TM3  
20 transmembrane domain deletion polypeptides are encompassed by the present  
invention: I1-S24, I1-V23, I1-F22, I1-N21, I1-I20, I1-A19, I1-A18, I1-Y17, I1-E16,  
I1-L15, I1-L14, I1-A13, I1-A12, I1-F11, I1-V10, I1-F9, I1-L8, and/or I1-L7 of SEQ  
ID NO:28. Polynucleotide sequences encoding these polypeptides are also provided.  
The present invention also encompasses the use of these C-terminal HGRA4sv TM3  
25 transmembrane domain deletion polypeptides as immunogenic and/or antigenic  
epitopes as described elsewhere herein.

HGRA4sv polypeptides and polynucleotides are useful for diagnosing diseases  
related to the over and/or under expression of HGRA4sv by identifying mutations in  
the HGRA4sv gene using HGRA4sv sequences as probes or by determining  
30 HGRA4sv protein or mRNA expression levels. HGRA4sv polypeptides will be useful  
in screens for compounds that affect the activity of the protein. HGRA4sv peptides  
can also be used for the generation of specific antibodies and as bait in yeast two  
hybrid screens to find proteins that specifically interact with HGRA4sv.

Expression profiling designed to measure the steady state mRNA levels  
35 encoding the HGRA4sv polypeptide showed predominately high expression levels in

5 heart and colon; significantly in uterus, and to a lesser extent, in testis and spinal cord (as shown in Figure 4).

Expanded analysis of HGPR4 expression levels by TaqMan™ quantitative PCR (see Figure 9) confirmed that the HGPR4 polypeptide is expressed in the lower gastrointestinal tract (duodenum, jejunum, caecum, colon and rectum). Additional, the 10 HGPR4 was also expressed significantly in the brain, dorsal root ganglia, pituitary, ovary and the uterus. These data suggest that HGPR4 would be useful for treating, detecting, and/or ameliorating disorders or diseases of the central and peripheral nervous system, including various types of syndromes that involve excitotoxic cell death and chronic peripheral neuropathies (neuropathic pain). HGRA4 may also play 15 a role in modulating longitudinal muscle/myenteric plexus contractions, and hence agonists or antagonists of HGRA4 could be used to treat various types of gastrointestinal disorders.

As described elsewhere herein, glycine receptor alpha subunits have been implicated in modulating inhibitory neurotransmission which is essential for 20 voluntary motor control, flex responses and sensory signal processing. Therefore, HGRA4sv polynucleotides and polypeptides of the present invention, including agonists and/or fragments thereof, have uses that include, modulating inhibitory neurotransmission which is essential for voluntary motor control, flex responses and sensory signal processing. Moreover, HGRA4sv polynucleotides and polypeptides of 25 the present invention, including agonists and/or fragments thereof, have uses that include, but are not limited to modulating neurite outgrowth, modulating the acrosome reaction, and preventing, ameliorating, and treating hyperplexia, spastic paraparesis, and memory deficit in inhibitory learning avoidance.

Depression is related to a decrease in neurotransmitter release. Current 30 treatments of depression include blockers of neurotransmitter uptake, and inhibitors of enzymes involved in neurotransmitter degradation which act to prolong the lifetime of neurotransmitters.

It is believed that certain diseases such as depression, memory disorders and Alzheimer's disease are the result of an impairment in neurotransmitter release.

35 Glycine receptor antagonists may therefore be utilized as cell excitants which may stimulate release of neurotransmitters such as acetylcholine, serotonin and dopamine.

5 Enhanced neurotransmitter release may reverse the symptoms associated with depression and Alzheimer's disease.

The HGRA4sv polynucleotides and polypeptides of the present invention, including agonists and/or fragments thereof, have uses that include modulating glycine receptor activity in various cells, tissues, and organisms, and particularly in 10 mammalian brain, heart, colon, uterus, testis, and spinal cord tissue, preferably human. HGRA4sv polynucleotides and polypeptides of the present invention, including agonists and/or fragments thereof, may be useful in diagnosing, treating, prognosing, and/or preventing cardiovascular, gastrointestinal, reproductive, and/or neural diseases or disorders.

15 The strong homology to human and mouse glycine receptor alpha subunit proteins, combined with the localized expression in heart suggests HGRA4sv polynucleotides and polypeptides of the present invention, including agonists and/or fragments thereof, may be useful in diagnosing, treating, prognosing, and/or preventing cardiovascular diseases and/or disorders, which include, but are not limited 20 to: myocardial infarction, congestive heart failure, arrhythmias, cardiomyopathy, atherosclerosis, arteriosclerosis, microvascular disease, embolism, thrombosis, pulmonary edema, palpitation, dyspnea, angina, hypotension, syncope, heart murmur, aberrant ECG, hypertrophic cardiomyopathy, the Marfan syndrome, sudden death, prolonged QT syndrome, congenital defects, cardiac viral infections, valvular heart 25 disease, hypertension,

Similarly, HGRA4sv polynucleotides and polypeptides may be useful for ameliorating cardiovascular diseases and symptoms which result indirectly from various non-cardiovascular effects, which include, but are not limited to, the following, obesity, smoking, Down syndrome (associated with endocardial cushion 30 defect); bony abnormalities of the upper extremities (associated with atrial septal defect in the Holt-Oram syndrome); muscular dystrophies (associated with cardiomyopathy); hemochromatosis and glycogen storage disease (associated with myocardial infiltration and restrictive cardiomyopathy); congenital deafness (associated with prolonged QT interval and serious cardiac arrhythmias); Raynaud's 35 disease (associated with primary pulmonary hypertension and coronary vasospasm); connective tissue disorders, i.e., the Marfan syndrome, Ehlers-Danlos and Hurler

5 syndromes, and related disorders of mucopolysaccharide metabolism (aortic dilatation, prolapsed mitral valve, a variety of arterial abnormalities); acromegaly (hypertension, accelerated coronary atherosclerosis, conduction defects, cardiomyopathy); hyperthyroidism (heart failure, atrial fibrillation); hypothyroidism (pericardial effusion, coronary artery disease); rheumatoid arthritis (pericarditis, aortic 10 valve disease); scleroderma (cor pulmonale, myocardial fibrosis, pericarditis); systemic lupus erythematosus (valvulitis, myocarditis, pericarditis); sarcoidosis (arrhythmias, cardiomyopathy); postmenopausal effects, Chlamydial infections, polycystic ovary disease, thyroid disease, alcoholism, diet, and exfoliative dermatitis (high-output heart failure), for example. Involvement of glycine receptors in 15 cardiovascular function has been previously reported (Kubo, T., Kihara, M, Neurosci, Lett., 74(3):331-6, (1987)).

Moreover, polynucleotides and polypeptides, including fragments and/or antagonists thereof, have uses which include, directly or indirectly, treating, preventing, diagnosing, and/or prognosing the following, non-limiting, cardiovascular 20 infections: blood stream invasion, bacteremia, sepsis, *Streptococcus pneumoniae* infection, group a streptococci infection, group b streptococci infection, *Enterococcus* infection, nonenterococcal group D streptococci infection, nonenterococcal group C streptococci infection, nonenterococcal group G streptococci infection, *Streptoccus viridans* infection, *Staphylococcus aureus* infection, coagulase-negative staphylococci 25 infection, gram-negative Bacilli infection, *Enterobacteriaceae* infection, *Psudomonas* spp. Infection, *Acinobacter* spp. Infection, *Flavobacterium meningosepticum* infection, *Aeromonas* spp. Infection, *Stenotrophomonas maltophilia* infection, gram-negative coccobacilli infection, *Haemophilus influenza* infection, *Branhamella catarrhalis* infection, anaerobe infection, *Bacteroides fragilis* infection, *Clostridium* 30 infection, fungal infection, *Candida* spp. Infection, non-albicans *Candida* spp. Infection, *Hansenula anomala* infection, *Malassezia furfur* infection, nontuberculous *Mycobacteria* infection, *Mycobacterium avium* infection, *Mycobacterium chelonae* infection, *Mycobacterium fortuitum* infection, spirochetal infection, *Borrelia burgdorferi* infection, in addition to any other cardiovascular disease and/or disorder 35 (e.g., non-sepsis) implicated by the causative agents listed above or elsewhere herein.

5        In addition, the strong homology to human and mouse glycine receptor alpha subunit proteins, combined with the localized expression in colon tissue, in addition to other gastrointestinal tissues, suggests the HGRA4sv polynucleotides and polypeptides may be useful in treating, diagnosing, prognosing, and/or preventing gastrointestinal diseases and/or disorders, which include, but are not limited to, ulcers,  
10      irritable bowel syndrome, inflammatory bowel disease, diarrhea, traveler's diarrhea, drug-related diarrhea polyps, absorption disorders, constipation, diverticulitis, vascular disease of the intestines, intestinal obstruction, intestinal infections, ulcerative colitis, Shigellosis, cholera, Crohn's Disease, amebiasis, enteric fever, Whipple's Disease, peritonitis, intrabdominal abscesses, hereditary hemochromatosis,  
15      gastroenteritis, viral gastroenteritis, food poisoning, mesenteric ischemia, mesenteric infarction, in addition to, metabolic diseases and/or disorders.

Moreover, polynucleotides and polypeptides, including fragments and/or antagonists thereof, have uses which include, directly or indirectly, treating, preventing, diagnosing, and/or prognosing susceptibility to the following, non-limiting, gastrointestinal infections: *Salmonella* infection, *E.coli* infection, *E.coli* O157:H7 infection, *Shiga Toxin*-producing *E.coli* infection, *Campylobacter* infection (e.g., *Campylobacter fetus*, *Campylobacter upsaliensis*, *Campylobacter hyoilealis*, *Campylobacter lari*, *Campylobacter jejuni*, *Campylobacter concisus*, *Campylobacter mucosalis*, *Campylobacter sputorum*, *Campylobacter rectus*,  
25      *Campylobacter curvus*, *Campylobacter sputorum*, etc.), *Helicobacter* infection (e.g., *Helicobacter cinaedi*, *Helicobacter fennelliae*, etc.) *Yersinia enterocolitica* infection, *Vibrio* sp. Infection (e.g., *Vibrio mimicus*, *Vibrio parahaemolyticus*, *Vibrio fluvialis*, *Vibrio furnissii*, *Vibrio hollisae*, *Vibrio vulnificus*, *Vibrio alginolyticus*, *Vibrio metschnikovii*, *Vibrio damsela*, *Vibrio cincinnatiensis*, etc.) *Aeromonas* infection  
30      (e.g., *Aeromonas hydrophila*, *Aeromonas sobria*, *Aeromonas caviae*, etc.), *Plesiomonas shigelloides* infection, *Giardia* infection (e.g., *Giardia lamblia*, etc.), *Cryptosporidium* infection, *Listeria* infection, *Entamoeba histolytica* infection, *Rotavirus* infection, *Norwalk* virus infection, *Clostridium difficile* infection, *Clostridium perfringens* infection, *Staphylococcus* infection, *Bacillus* infection, in  
35      addition to any other gastrointestinal disease and/or disorder implicated by the causative agents listed above or elsewhere herein.

5 In addition, antagonists of the HGRA4sv polynucleotides and polypeptides may have uses that include diagnosing, treating, prognosing, and/or preventing diseases or disorders related to hyper glycine receptor alpha subunit activity, which may include cardiovascular, gastrointestinal, reproductive, neural, and/or proliferative diseases or disorders.

10 Although it is believed the encoded polypeptide may share at least some biological activities with glycine receptor alpha subunits, a number of methods of determining the exact biological function of this clone are either known in the art or are described elsewhere herein. Briefly, the function of this clone may be determined by applying microarray methodology. Nucleic acids corresponding to the HGRA4sv 15 polynucleotides, in addition to, other clones of the present invention, may be arrayed on microchips for expression profiling. Depending on which polynucleotide probe is used to hybridize to the slides, a change in expression of a specific gene may provide additional insight into the function of this gene based upon the conditions being studied. For example, an observed increase or decrease in expression levels when the 20 polynucleotide probe used comes from tissue that has been treated with known glycine receptor inhibitors, which include, but are not limited to the drugs listed above, might indicate a function in modulating glycine receptor function, for example. In the case of HGRA4sv, brain, heart, colon, uterus, testis, and/or spinal cord tissue should be used to extract RNA to prepare the probe.

25 In addition, the function of the protein may be assessed by applying quantitative PCR methodology, for example. Real time quantitative PCR would provide the capability of following the expression of the HGRA4sv gene throughout development, for example. Quantitative PCR methodology requires only a nominal amount of tissue from each developmentally important step is needed to perform such 30 experiments. Therefore, the application of quantitative PCR methodology to refining the biological function of this polypeptide is encompassed by the present invention. Also encompassed by the present invention are quantitative PCR probes corresponding to the polynucleotide sequence provided as SEQ ID NO:3 (Figures 2A-B).

35 The function of the protein may also be assessed through complementation assays in yeast. For example, in the case of the HGRA4sv, transforming yeast

5 deficient in glycine receptor alpha subunit activity and assessing their ability to grow would provide convincing evidence the HGRA4sv polypeptide has glycine receptor alpha subunit activity. Additional assay conditions and methods that may be used in assessing the function of the polynucleotides and polypeptides of the present invention are known in the art, some of which are disclosed elsewhere herein.

10 Alternatively, the biological function of the encoded polypeptide may be determined by disrupting a homologue of this polypeptide in Mice and/or rats and observing the resulting phenotype.

Moreover, the biological function of this polypeptide may be determined by the application of antisense and/or sense methodology and the resulting generation of 15 transgenic mice and/or rats. Expressing a particular gene in either sense or antisense orientation in a transgenic mouse or rat could lead to respectively higher or lower expression levels of that particular gene. Altering the endogenous expression levels of a gene can lead to the observation of a particular phenotype that can then be used to derive indications on the function of the gene. The gene can be either over-expressed 20 or under expressed in every cell of the organism at all times using a strong ubiquitous promoter, or it could be expressed in one or more discrete parts of the organism using a well characterized tissue-specific promoter (e.g., a brain, heart, colon, uterus, testis, or spinal cord-specific promoter), or it can be expressed at a specified time of development using an inducible and/or a developmentally regulated promoter.

25 In the case of HGRA4sv transgenic mice or rats, if no phenotype is apparent in normal growth conditions, observing the organism under diseased conditions (cardiovascular, gastrointestinal, reproductive, neural, or proliferative disorders, etc.) may lead to understanding the function of the gene. Therefore, the application of antisense and/or sense methodology to the creation of transgenic mice or rats to refine 30 the biological function of the polypeptide is encompassed by the present invention.

In preferred embodiments, the following N-terminal HGRA4sv deletion polypeptides are encompassed by the present invention: M1-D431, T2-D431, T3-D431, L4-D431, V5-D431, P6-D431, A7-D431, T8-D431, L9-D431, S10-D431, F11-D431, L12-D431, L13-D431, L14-D431, W15-D431, T16-D431, L17-D431, P18-D431, G19-D431, Q20-D431, V21-D431, L22-D431, L23-D431, R24-D431, V25-D431, A26-D431, L27-D431, A28-D431, K29-D431, E30-D431, E31-D431, V32-

5 D431, K33-D431, S34-D431, G35-D431, T36-D431, K37-D431, G38-D431, S39-  
D431, Q40-D431, P41-D431, M42-D431, S43-D431, P44-D431, S45-D431, D46-  
D431, F47-D431, L48-D431, D49-D431, K50-D431, L51-D431, M52-D431, G53-  
D431, R54-D431, T55-D431, S56-D431, G57-D431, Y58-D431, D59-D431, A60-  
D431, R61-D431, I62-D431, R63-D431, P64-D431, N65-D431, F66-D431, K67-  
10 D431, G68-D431, P69-D431, P70-D431, V71-D431, N72-D431, V73-D431, T74-  
D431, C75-D431, N76-D431, I77-D431, F78-D431, I79-D431, N80-D431, S81-  
D431, F82-D431, S83-D431, S84-D431, V85-D431, T86-D431, K87-D431, T88-  
D431, T89-D431, M90-D431, D91-D431, Y92-D431, R93-D431, V94-D431, N95-  
D431, V96-D431, F97-D431, L98-D431, R99-D431, Q100-D431, Q101-D431,  
15 W102-D431, N103-D431, D104-D431, P105-D431, R106-D431, L107-D431, S108-  
D431, Y109-D431, R110-D431, E111-D431, Y112-D431, P113-D431, D114-D431,  
D115-D431, S116-D431, L117-D431, D118-D431, L119-D431, D120-D431, P121-  
D431, S122-D431, M123-D431, L124-D431, D125-D431, S126-D431, I127-D431,  
W128-D431, K129-D431, P130-D431, D131-D431, L132-D431, F133-D431, F134-  
20 D431, A135-D431, N136-D431, E137-D431, K138-D431, G139-D431, A140-D431,  
N141-D431, F142-D431, H143-D431, E144-D431, V145-D431, T146-D431, T147-  
D431, D148-D431, N149-D431, K150-D431, L151-D431, L152-D431, R153-D431,  
I154-D431, F155-D431, K156-D431, N157-D431, G158-D431, N159-D431, V160-  
D431, L161-D431, Y162-D431, S163-D431, I164-D431, R165-D431, L166-D431,  
25 T167-D431, L168-D431, I169-D431, L170-D431, S171-D431, C172-D431, L173-  
D431, M174-D431, D175-D431, L176-D431, K177-D431, N178-D431, F179-D431,  
P180-D431, M181-D431, D182-D431, I183-D431, Q184-D431, T185-D431, C186-  
D431, T187-D431, M188-D431, Q189-D431, L190-D431, E191-D431, S192-D431,  
S193-D431, S194-D431, I195-D431, L196-D431, C197-D431, S198-D431, P199-  
30 D431, L200-D431, P201-D431, S202-D431, L203-D431, S204-D431, L205-D431,  
S206-D431, V207-D431, G208-D431, Y209-D431, T210-D431, M211-D431, K212-  
D431, D213-D431, L214-D431, V215-D431, F216-D431, E217-D431, W218-D431,  
L219-D431, E220-D431, D221-D431, A222-D431, P223-D431, A224-D431, V225-  
D431, Q226-D431, V227-D431, A228-D431, E229-D431, G230-D431, L231-D431,  
35 T232-D431, L233-D431, P234-D431, Q235-D431, F236-D431, I237-D431, L238-  
D431, R239-D431, D240-D431, E241-D431, K242-D431, D243-D431, L244-D431,

5    G245-D431, C246-D431, C247-D431, T248-D431, K249-D431, H250-D431, Y251-  
D431, N252-D431, T253-D431, G254-D431, K255-D431, F256-D431, T257-D431,  
C258-D431, I259-D431, E260-D431, V261-D431, K262-D431, F263-D431, H264-  
D431, L265-D431, E266-D431, R267-D431, Q268-D431, M269-D431, G270-D431,  
Y271-D431, Y272-D431, L273-D431, I274-D431, Q275-D431, M276-D431, Y277-  
10   D431, I278-D431, P279-D431, S280-D431, L281-D431, L282-D431, I283-D431,  
V284-D431, I285-D431, L286-D431, S287-D431, W288-D431, V289-D431, S290-  
D431, F291-D431, W292-D431, I293-D431, N294-D431, M295-D431, D296-D431,  
A297-D431, A298-D431, P299-D431, A300-D431, R301-D431, V302-D431, G303-  
D431, L304-D431, G305-D431, I306-D431, T307-D431, T308-D431, V309-D431,  
15   L310-D431, T311-D431, M312-D431, T313-D431, T314-D431, Q315-D431, S316-  
D431, S317-D431, G318-D431, S319-D431, R320-D431, A321-D431, S322-D431,  
L323-D431, P324-D431, K325-D431, V326-D431, S327-D431, Y328-D431, V329-  
D431, K330-D431, A331-D431, I332-D431, D333-D431, I334-D431, W335-D431,  
M336-D431, A337-D431, V338-D431, C339-D431, L340-D431, L341-D431, F342-  
20   D431, V343-D431, F344-D431, A345-D431, A346-D431, L347-D431, L348-D431,  
E349-D431, Y350-D431, A351-D431, A352-D431, I353-D431, N354-D431, F355-  
D431, V356-D431, S357-D431, R358-D431, Q359-D431, H360-D431, K361-D431,  
E362-D431, F363-D431, I364-D431, R365-D431, L366-D431, R367-D431, R368-  
D431, R369-D431, Q370-D431, R371-D431, R372-D431, Q373-D431, R374-D431,  
25   L375-D431, E376-D431, E377-D431, D378-D431, I379-D431, I380-D431, Q381-  
D431, E382-D431, S383-D431, R384-D431, F385-D431, Y386-D431, F387-D431,  
R388-D431, G389-D431, Y390-D431, G391-D431, L392-D431, G393-D431, H394-  
D431, C395-D431, L396-D431, Q397-D431, A398-D431, R399-D431, D400-D431,  
G401-D431, G402-D431, P403-D431, M404-D431, E405-D431, G406-D431, S407-  
30   D431, G408-D431, I409-D431, Y410-D431, S411-D431, P412-D431, Q413-D431,  
P414-D431, P415-D431, A416-D431, P417-D431, L418-D431, L419-D431, R420-  
D431, E421-D431, G422-D431, E423-D431, T424-D431, and/or T425-D431 of SEQ  
ID NO:4. Polynucleotide sequences encoding these polypeptides are also provided.  
The present invention also encompasses the use of these N-terminal HGRA4sv  
35   deletion polypeptides as immunogenic and/or antigenic epitopes as described  
elsewhere herein.

5 In preferred embodiments, the following C-terminal HGRA4sv deletion polypeptides are encompassed by the present invention: M1-D431, M1-V430, M1-Y429, M1-L428, M1-K427, M1-R426, M1-T425, M1-T424, M1-E423, M1-G422, M1-E421, M1-R420, M1-L419, M1-L418, M1-P417, M1-A416, M1-P415, M1-P414, M1-Q413, M1-P412, M1-S411, M1-Y410, M1-I409, M1-G408, M1-S407, M1-G406, 10 M1-E405, M1-M404, M1-P403, M1-G402, M1-G401, M1-D400, M1-R399, M1-A398, M1-Q397, M1-L396, M1-C395, M1-H394, M1-G393, M1-L392, M1-G391, M1-Y390, M1-G389, M1-R388, M1-F387, M1-Y386, M1-F385, M1-R384, M1-S383, M1-E382, M1-Q381, M1-I380, M1-I379, M1-D378, M1-E377, M1-E376, M1-L375, M1-R374, M1-Q373, M1-R372, M1-R371, M1-Q370, M1-R369, M1-R368, 15 M1-R367, M1-L366, M1-R365, M1-I364, M1-F363, M1-E362, M1-K361, M1-H360, M1-Q359, M1-R358, M1-S357, M1-V356, M1-F355, M1-N354, M1-I353, M1-A352, M1-A351, M1-Y350, M1-E349, M1-L348, M1-L347, M1-A346, M1-A345, M1-F344, M1-V343, M1-F342, M1-L341, M1-L340, M1-C339, M1-V338, M1-A337, M1-M336, M1-W335, M1-I334, M1-D333, M1-I332, M1-A331, M1-K330, M1- 20 V329, M1-Y328, M1-S327, M1-V326, M1-K325, M1-P324, M1-L323, M1-S322, M1-A321, M1-R320, M1-S319, M1-G318, M1-S317, M1-S316, M1-Q315, M1-T314, M1-T313, M1-M312, M1-T311, M1-L310, M1-V309, M1-T308, M1-T307, M1-I306, M1-G305, M1-L304, M1-G303, M1-V302, M1-R301, M1-A300, M1-P299, M1-A298, M1-A297, M1-D296, M1-M295, M1-N294, M1-I293, M1-W292, M1- 25 F291, M1-S290, M1-V289, M1-W288, M1-S287, M1-L286, M1-I285, M1-V284, M1-I283, M1-L282, M1-L281, M1-S280, M1-P279, M1-I278, M1-Y277, M1-M276, M1-Q275, M1-I274, M1-L273, M1-Y272, M1-Y271, M1-G270, M1-M269, M1-Q268, M1-R267, M1-E266, M1-L265, M1-H264, M1-F263, M1-K262, M1-V261, M1-E260, M1-I259, M1-C258, M1-T257, M1-F256, M1-K255, M1-G254, M1-T253, 30 M1-N252, M1-Y251, M1-H250, M1-K249, M1-T248, M1-C247, M1-C246, M1-G245, M1-L244, M1-D243, M1-K242, M1-E241, M1-D240, M1-R239, M1-L238, M1-I237, M1-F236, M1-Q235, M1-P234, M1-L233, M1-T232, M1-L231, M1-G230, M1-E229, M1-A228, M1-V227, M1-Q226, M1-V225, M1-A224, M1-P223, M1-A222, M1-D221, M1-E220, M1-L219, M1-W218, M1-E217, M1-F216, M1-V215, 35 M1-L214, M1-D213, M1-K212, M1-M211, M1-T210, M1-Y209, M1-G208, M1-V207, M1-S206, M1-L205, M1-S204, M1-L203, M1-S202, M1-P201, M1-L200, M1-

5 P199, M1-S198, M1-C197, M1-L196, M1-I195, M1-S194, M1-S193, M1-S192, M1-  
E191, M1-L190, M1-Q189, M1-M188, M1-T187, M1-C186, M1-T185, M1-Q184,  
M1-I183, M1-D182, M1-M181, M1-P180, M1-F179, M1-N178, M1-K177, M1-  
L176, M1-D175, M1-M174, M1-L173, M1-C172, M1-S171, M1-L170, M1-I169,  
M1-L168, M1-T167, M1-L166, M1-R165, M1-I164, M1-S163, M1-Y162, M1-L161,  
10 M1-V160, M1-N159, M1-G158, M1-N157, M1-K156, M1-F155, M1-I154, M1-  
R153, M1-L152, M1-L151, M1-K150, M1-N149, M1-D148, M1-T147, M1-T146,  
M1-V145, M1-E144, M1-H143, M1-F142, M1-N141, M1-A140, M1-G139, M1-  
K138, M1-E137, M1-N136, M1-A135, M1-F134, M1-F133, M1-L132, M1-D131,  
M1-P130, M1-K129, M1-W128, M1-I127, M1-S126, M1-D125, M1-L124, M1-  
15 M123, M1-S122, M1-P121, M1-D120, M1-L119, M1-D118, M1-L117, M1-S116,  
M1-D115, M1-D114, M1-P113, M1-Y112, M1-E111, M1-R110, M1-Y109, M1-  
S108, M1-L107, M1-R106, M1-P105, M1-D104, M1-N103, M1-W102, M1-Q101,  
M1-Q100, M1-R99, M1-L98, M1-F97, M1-V96, M1-N95, M1-V94, M1-R93, M1-  
Y92, M1-D91, M1-M90, M1-T89, M1-T88, M1-K87, M1-T86, M1-V85, M1-S84,  
20 M1-S83, M1-F82, M1-S81, M1-N80, M1-I79, M1-F78, M1-I77, M1-N76, M1-C75,  
M1-T74, M1-V73, M1-N72, M1-V71, M1-P70, M1-P69, M1-G68, M1-K67, M1-  
F66, M1-N65, M1-P64, M1-R63, M1-I62, M1-R61, M1-A60, M1-D59, M1-Y58,  
M1-G57, M1-S56, M1-T55, M1-R54, M1-G53, M1-M52, M1-L51, M1-K50, M1-  
D49, M1-L48, M1-F47, M1-D46, M1-S45, M1-P44, M1-S43, M1-M42, M1-P41,  
25 M1-Q40, M1-S39, M1-G38, M1-K37, M1-T36, M1-G35, M1-S34, M1-K33, M1-  
V32, M1-E31, M1-E30, M1-K29, M1-A28, M1-L27, M1-A26, M1-V25, M1-R24,  
M1-L23, M1-L22, M1-V21, M1-Q20, M1-G19, M1-P18, M1-L17, M1-T16, M1-  
W15, M1-L14, M1-L13, M1-L12, M1-F11, M1-S10, M1-L9, M1-T8, and/or M1-A7  
of SEQ ID NO:4. Polynucleotide sequences encoding these polypeptides are also  
30 provided. The present invention also encompasses the use of these C-terminal  
HGRA4sv deletion polypeptides as immunogenic and/or antigenic epitopes as  
described elsewhere herein.

Alternatively, preferred polypeptides of the present invention may comprise  
polypeptide sequences corresponding to, for example, internal regions of the  
35 HGRA4sv polypeptide (e.g., any combination of both N- and C- terminal HGRA4sv  
polypeptide deletions) of SEQ ID NO:4. For example, internal regions could be

5 defined by the equation: amino acid NX to amino acid CX, wherein NX refers to any  
N-terminal deletion polypeptide amino acid of HGRA4sv (SEQ ID NO:4), and where  
CX refers to any C-terminal deletion polypeptide amino acid of HGRA4sv (SEQ ID  
NO:4). Polynucleotides encoding these polypeptides are also provided. The present  
invention also encompasses the use of these polypeptides as an immunogenic and/or  
10 antigenic epitope as described elsewhere herein.

The HGRA4sv polypeptide of the present invention was determined to comprise a neurotransmitter gated ion channel domain from about amino acid 44 to about amino acid 355 of SEQ ID NO:4 (Figures 2A-B) according to the Pfam domain analysis algorithm (Bateman, A., Birney, E. R., Durbin, S. R., Eddy,  
15 S. R., Howe, K. L., and Sonnhammer, E. L. L., Nucleic Acids Research 28, 263-266  
(2000)). In this context, the term “about” should be construed to mean 1, 2, 3, 4, 5, 6,  
7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 more amino acids in either the N-  
or C-terminal direction of the above referenced polypeptide. Polynucleotides  
encoding these polypeptides are also provided.

20 Neurotransmitter-gated ion channels are transmembrane receptor-ion channel complexes that open transiently upon binding of specific ligands, allowing rapid transmission of signals at chemical synapses.

Of the five families known, four have been shown to form a sequence-related super-family. These are the gamma-aminobutyric acid type A(GABA-A), nicotinic  
25 acetylcholine, glycine and the serotonin 5HT3 receptors. The ionotropic glutamate receptors have a distinct primary structure.

However, all these receptors possess a pentameric structure (made up of varying subunits), surrounding a central pore. Each of these subunits contains a large extracellular N-terminal ligand-binding region; 3 hydrophobic transmembrane  
30 domains; a large intracellular region; and a fourth hydrophobic domain. Such a domain may also be required for the HGRA4sv alpha subunits ability to modulate neurotransmitter transmission.

Preferred polypeptides of the invention comprise the following amino acid sequence:

35 PSDFLDKLMGRTSGYDARIRPNFKGPPVNVCNIFINSFSSVTKTMDYRVNV  
FLRQQWNDPRLSYREYPDDSLDDPSMLDSIWKPDLFFANEKGANFHEVTD

5 NKLLRIFKNGNVLYSIRTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSL  
SLSVGYTMKDLVFEWLEDAPAVQVAEGLTPQFILRDEKDLGCCTKHYNTG  
KFTCIEVKFHLLRQMGYYLIQMYIPSLLIVLSWVSWINMDAAPARVGLGITT  
VLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINF (SEQ ID  
NO:15). Polynucleotides encoding these polypeptides are also provided. The present  
10 invention also encompasses the use of this HGRA4sv neurotransmitter gated ion  
channel domain polypeptides as immunogenic and/or antigenic epitopes as  
described elsewhere herein.

The HGRA4sv polypeptides of the present invention were determined to  
comprise several phosphorylation sites based upon the Motif algorithm (Genetics  
15 Computer Group, Inc.). The phosphorylation of such sites may regulate some  
biological activity of the HGRA4sv polypeptide. For example, phosphorylation at  
specific sites may be involved in regulating the protein's ability to associate or bind to  
other molecules (e.g., proteins, ligands, substrates, DNA, etc.). In the present case,  
phosphorylation may modulate the ability of the HGRA4sv polypeptide to associate  
20 with other potassium channel alpha subunits, beta subunits, or its ability to modulate  
potassium channel function.

The HGRA4sv polypeptide was predicted to comprise six PKC  
phosphorylation sites using the Motif algorithm (Genetics Computer Group, Inc.). In  
vivo, protein kinase C exhibits a preference for the phosphorylation of serine or  
25 threonine residues. The PKC phosphorylation sites have the following consensus  
pattern: [ST]-x-[RK], where S or T represents the site of phosphorylation and 'x' an  
intervening amino acid residue. Additional information regarding PKC  
phosphorylation sites can be found in Woodget J.R., Gould K.L., Hunter T., Eur. J.  
Biochem. 161:177-184(1986), and Kishimoto A., Nishiyama K., Nakanishi H.,  
30 Uratsuji Y., Nomura H., Takeyama Y., Nishizuka Y., J. Biol. Chem. 260:12492-  
12499(1985); which are hereby incorporated by reference herein.

In preferred embodiments, the following PKC phosphorylation site  
polypeptides are encompassed by the present invention: NDPRLSYREYPDD (SEQ  
ID NO:30), GNVLYSIRTLIL (SEQ ID NO:31), LSVGYTMKDLVFE (SEQ ID  
35 NO:32), TKHYNTGKFTCIE (SEQ ID NO:33), LREGETTRKLYVD (SEQ ID

5 NO:34), and/or REGETTRKLYVD (SEQ ID NO:35). Polynucleotides encoding these polypeptides are also provided.

The present invention also encompasses immunogenic and/or antigenic epitopes of the HGRA4sv polypeptide.

The HGRA4sv polypeptide has been shown to comprise one glycosylation site 10 according to the Motif algorithm (Genetics Computer Group, Inc.). As discussed more specifically herein, protein glycosylation is thought to serve a variety of functions including: augmentation of protein folding, inhibition of protein aggregation, regulation of intracellular trafficking to organelles, increasing resistance to proteolysis, modulation of protein antigenicity, and mediation of intercellular 15 adhesion.

Asparagine phosphorylation sites have the following consensus pattern, N-{P}-[ST]-{P}, wherein N represents the glycosylation site. However, it is well known that that potential N-glycosylation sites are specific to the consensus sequence Asn-Xaa-Ser/Thr. However, the presence of the consensus tripeptide is not sufficient to 20 conclude that an asparagine residue is glycosylated, due to the fact that the folding of the protein plays an important role in the regulation of N-glycosylation. It has been shown that the presence of proline between Asn and Ser/Thr will inhibit N-glycosylation; this has been confirmed by a recent statistical analysis of glycosylation sites, which also shows that about 50% of the sites that have a proline C-terminal to 25 Ser/Thr are not glycosylated. Additional information relating to asparagine glycosylation may be found in reference to the following publications, which are hereby incorporated by reference herein: Marshall R.D., Annu. Rev. Biochem. 41:673-702(1972); Pless D.D., Lennarz W.J., Proc. Natl. Acad. Sci. U.S.A. 74:134-138(1977); Bause E., Biochem. J. 209:331-336(1983); Gavel Y., von Heijne G., 30 Protein Eng. 3:433-442(1990); and Miletich J.P., Broze G.J. Jr., J. Biol. Chem. 265:11397-11404(1990).

In preferred embodiments, the following asparagine glycosylation site polypeptides are encompassed by the present invention: KGPPVNVTNCNIFIN (SEQ ID NO:29). Polynucleotides encoding these polypeptides are also provided. The 35 present invention also encompasses the use of these HGRA4sv asparagine

5 glycosylation site polypeptides as immunogenic and/or antigenic epitopes as described elsewhere herein.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:3 and may have been publicly available prior to conception of 10 the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides consisting of a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1626 of SEQ ID NO:3, b 15 is an integer between 15 to 1640, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:3, and where b is greater than or equal to a+14.

**Table I**

Gene No.	CDNA CloneID	ATCC Deposit No. Z and Date	Vector	NT SEQ ID. No. X	Total NT Seq of Clone	5' NT of Start Codon of ORF	3' NT of ORF	AA Seq ID No. Y	Total AA of ORF
1.	HGRA4 (clone E3)	XXXXX Xx/Xx/Xx	PsportI	1	2565	1	1251	2	417
2.	HGRA4sv (clone D8)	PTA-2966 01/24/01	PsportI	3	1640	1	1293	4	431

20

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the 25 "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually several overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding 30 deposit number listed in "ATCC Deposit No:Z and Date." "Vector" refers to the type of vector contained in the cDNA Clone ID.

5 "Total NT Seq. Of Clone" refers to the total number of nucleotides in the clone contig identified by "Gene No." The deposited clone may contain all or most of the sequence of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon of ORF."

10 The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

15 The total number of amino acids within the open reading frame of SEQ ID NO:Y is identified as "Total AA of ORF".

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing) and the translated SEQ ID NO:Y (where Y may be any of the polypeptide sequences disclosed in the sequence listing) are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and 20 described further herein. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ 25 ID NO:Y may be used, for example, to generate antibodies which bind specifically to proteins containing the polypeptides and the proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or 30 deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides may cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base 35 insertion or deletion in an open reading frame of over 1000 bases).

5        Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. 20 Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs, allelic variants, and/or orthologs. The skilled artisan could, using procedures well-known in the art, 25 obtain the polynucleotide sequence corresponding to full-length genes (including, but not limited to the full-length coding region), allelic variants, splice variants, orthologs, and/or species homologues of genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or a deposited clone, relying on the sequence from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species 30 homologues may be isolated and identified by making suitable probes or primers which correspond to the 5', 3', or internal regions of the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. 35 Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides

5 produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

10 The polypeptides may be in the form of the protein, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-  
15 sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

15 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using protocols described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the full-length form of the protein.

20 The present invention provides a polynucleotide comprising, or alternatively consisting of, the sequence identified as SEQ ID NO:X, and/or a cDNA provided in ATCC Deposit No. Z:. The present invention also provides a polypeptide comprising, or alternatively consisting of, the sequence identified as SEQ ID NO:Y, and/or a polypeptide encoded by the cDNA provided in ATCC Deposit NO:Z. The present  
25 invention also provides polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, and/or a polypeptide sequence encoded by the cDNA contained in ATCC Deposit No:Z.

30 Preferably, the present invention is directed to a polynucleotide comprising, or alternatively consisting of, the sequence identified as SEQ ID NO:X, and/or a cDNA provided in ATCC Deposit No.: that is less than, or equal to, a polynucleotide sequence that is 5 mega basepairs, 1 mega basepairs, 0.5 mega basepairs, 0.1 mega basepairs, 50,000 basepairs, 20,000 basepairs, or 10,000 basepairs in length.

35 The present invention encompasses polynucleotides with sequences complementary to those of the polynucleotides of the present invention disclosed herein. Such sequences may be complementary to the sequence disclosed as SEQ ID

5 NO:X, the sequence contained in a deposit, and/or the nucleic acid sequence encoding the sequence disclosed as SEQ ID NO:Y.

The present invention also encompasses polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions, and most preferably under highly stringent conditions, to 10 polynucleotides described herein. Examples of stringency conditions are shown in Table 2 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

5 TABLE 2

Stringency Condition	Polynucleotide Hybrid±	Hybrid Length (bp) ‡	Hyridization Temperature and Buffer†	Wash Temperature and Buffer †
A	DNA:DNA	> or equal to 50	65°C; 1xSSC —or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
B	DNA:DNA	< 50	Tb*; 1xSSC	Tb*; 1xSSC
C	DNA:RNA	> or equal to 50	67°C; 1xSSC —or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
D	DNA:RNA	< 50	Td*; 1xSSC	Td*; 1xSSC
E	RNA:RNA	> or equal to 50	70°C; 1xSSC —or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
F	RNA:RNA	< 50	Tf*; 1xSSC	Tf*; 1xSSC
G	DNA:DNA	> or equal to 50	65°C; 4xSSC —or- 45°C; 4xSSC, 50% formamide	65°C; 1xSSC
H	DNA:DNA	< 50	Th*; 4xSSC	Th*; 4xSSC
I	DNA:RNA	> or equal to 50	67°C; 4xSSC —or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
J	DNA:RNA	< 50	Tj*; 4xSSC	Tj*; 4xSSC
K	RNA:RNA	> or equal to 50	70°C; 4xSSC —or- 40°C; 6xSSC, 50% formamide	67°C; 1xSSC
L	RNA:RNA	< 50	Tl*; 2xSSC	Tl*; 2xSSC
M	DNA:DNA	> or equal to 50	50°C; 4xSSC —or- 40°C 6xSSC, 50% formamide	50°C; 2xSSC
N	DNA:DNA	< 50	Tn*; 6xSSC	Tn*; 6xSSC
O	DNA:RNA	> or equal to 50	55°C; 4xSSC —or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
P	DNA:RNA	< 50	Tp*; 6xSSC	Tp*; 6xSSC
Q	RNA:RNA	> or equal to 50	60°C; 4xSSC —or-	60°C; 2xSSC

Stringency Condition	Polynucleotide Hybrid $\pm$	Hybrid Length (bp) $\ddagger$	Hybridization Temperature and Buffer $\ddagger$	Wash Temperature and Buffer $\ddagger$
			45°C; 6xSSC, 50% formamide	
R	RNA:RNA	< 50	Tr*; 4xSSC	Tr*; 4xSSC

5

‡ - The "hybrid length" is the anticipated length for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide of unknown sequence, the hybrid is assumed to be that of the hybridizing polynucleotide of the present invention. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity. Methods of aligning two or more polynucleotide sequences and/or determining the percent identity between two polynucleotide sequences are well known in the art (e.g., 10 MegAlign program of the DNA\*Star suite of programs, etc).

15       † - SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete. The hybridizations and washes may additionally include 20 5X Denhardt's reagent, .5-1.0% SDS, 100ug/ml denatured, fragmented salmon sperm DNA, 0.5% sodium pyrophosphate, and up to 50% formamide.

25       \*Tb - Tr: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature T<sub>m</sub> of the hybrids. There T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = .165 M).

30       ± - The present invention encompasses the substitution of any one, or more DNA or RNA hybrid partners with either a PNA, or a modified polynucleotide. Such

5 modified polynucleotides are known in the art and are more particularly described elsewhere herein.

Additional examples of stringency conditions for polynucleotide hybridization are provided, for example, in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, 10 Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M., Ausubel et al., eds, John Wiley and Sons, Inc., sections 2.10 and 6.3-6.4, which are hereby incorporated by reference herein.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; and most preferably at least 90% or 15 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The determination of identity is well known in the art, and discussed more specifically elsewhere herein.

20 The invention encompasses the application of PCR methodology to the polynucleotide sequences of the present invention, the clone deposited with the ATCC, and/or the cDNA encoding the polypeptides of the present invention. PCR techniques for the amplification of nucleic acids are described in US Patent No. 4, 683, 195 and Saiki et al., Science, 239:487-491 (1988). PCR, for example, may 25 include the following steps, of denaturation of template nucleic acid (if double-stranded), annealing of primer to target, and polymerization. The nucleic acid probed or used as a template in the amplification reaction may be genomic DNA, cDNA, RNA, or a PNA. PCR may be used to amplify specific sequences from genomic DNA, specific RNA sequence, and/or cDNA transcribed from mRNA. References for 30 the general use of PCR techniques, including specific method parameters, include Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, (1987), Ehrlich (ed), PCR Technology, Stockton Press, NY, 1989; Ehrlich et al., Science, 252:1643-1650, (1991); and "PCR Protocols, A Guide to Methods and Applications", Eds., Innis et al., Academic Press, New York, (1990).

### Polynucleotide and Polypeptide Variants

The present invention also encompasses variants (e.g., allelic variants, orthologs, etc.) of the polynucleotide sequence disclosed herein in SEQ ID NO:X, the complementary strand thereto, and/or the cDNA sequence contained in the deposited 10. clone.

The present invention also encompasses variants of the polypeptide sequence, and/or fragments therein, disclosed in SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide encoded by a cDNA in the deposited clone.

15 "Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

Thus, one aspect of the invention provides an isolated nucleic acid molecule 20 comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a HGRA4 related polypeptide having an amino acid sequence as shown in the sequence listing and described in SEQ ID NO:X or the cDNA contained in ATCC deposit No:PTA-2966; (b) a nucleotide sequence encoding a mature HGRA4 related 25 polypeptide having the amino acid sequence as shown in the sequence listing and described in SEQ ID NO:X or the cDNA contained in ATCC deposit No:PTA-2966; (c) a nucleotide sequence encoding a biologically active fragment of a HGRA4 related polypeptide having an amino acid sequence shown in the sequence listing and described in SEQ ID NO:X or the cDNA contained in ATCC deposit No:PTA-2966; 30 (d) a nucleotide sequence encoding an antigenic fragment of a HGRA4 related polypeptide having an amino acid sequence shown in the sequence listing and described in SEQ ID NO:X or the cDNA contained in ATCC deposit No:PTA-2966; (e) a nucleotide sequence encoding a HGRA4 related polypeptide comprising the complete amino acid sequence encoded by a human cDNA plasmid contained in 35 SEQ ID NO:X or the cDNA contained in ATCC deposit No:PTA-2966; (f) a nucleotide sequence encoding a mature HGRA4 related polypeptide having an amino

5 acid sequence encoded by a human cDNA plasmid contained in SEQ ID NO:X or the cDNA contained in ATCC deposit No:PTA-2966; (g) a nucleotide sequence encoding a biologically active fragment of a HGRA4 related polypeptide having an amino acid sequence encoded by a human cDNA plasmid contained in SEQ ID NO:X or the cDNA contained in ATCC deposit No:PTA-2966; (h) a nucleotide sequence encoding

10 an antigenic fragment of a HGRA4 related polypeptide having an amino acid sequence encoded by a human cDNA plasmid contained in SEQ ID NO:X or the cDNA contained in ATCC deposit No:PTA-2966; (I) a nucleotide sequence complimentary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), or (h), above.

15 The present invention is also directed to polynucleotide sequences which comprise, or alternatively consist of, a polynucleotide sequence which is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, or 99.9% identical to, for example, any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), or (h), above.

20 Polynucleotides encoded by these nucleic acid molecules are also encompassed by the invention. In another embodiment, the invention encompasses nucleic acid molecule which comprise, or alternatively, consist of a polynucleotide which hybridizes under stringent conditions, or alternatively, under lower stringency conditions, to a polynucleotide in (a), (b), (c), (d), (e), (f), (g), or (h), above. Polynucleotides which

25 hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polypeptides.

Another aspect of the invention provides an isolated nucleic acid molecule comprising, or alternatively, consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a HGRA4 related polypeptide having an amino acid sequence as shown in the sequence listing and described in Table 1; (b) a nucleotide sequence encoding a mature HGRA4 related polypeptide having the amino acid sequence as shown in the sequence listing and described in Table 1; (c) a nucleotide sequence encoding a biologically active fragment of a HGRA4 related polypeptide having an amino acid sequence as shown in the sequence listing and described in Table 1; (d) a nucleotide sequence encoding

5 an antigenic fragment of a HGRA4 related polypeptide having an amino acid sequence as shown in the sequence listing and described in Table 1; (e) a nucleotide sequence encoding a HGRA4 related polypeptide comprising the complete amino acid sequence encoded by a human cDNA in a cDNA plasmid contained in the ATCC Deposit and described in Table 1; (f) a nucleotide sequence encoding a mature

10 HGRA4 related polypeptide having an amino acid sequence encoded by a human cDNA in a cDNA plasmid contained in the ATCC Deposit and described in Table 1; (g) a nucleotide sequence encoding a biologically active fragment of a HGRA4 related polypeptide having an amino acid sequence encoded by a human cDNA in a cDNA plasmid contained in the ATCC Deposit and described in Table 1; (h) a

15 nucleotide sequence encoding an antigenic fragment of a HGRA4 related polypeptide having an amino acid sequence encoded by a human cDNA in a cDNA plasmid contained in the ATCC deposit and described in Table 1; (i) a nucleotide sequence complimentary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), or (h) above.

20 The present invention is also directed to nucleic acid molecules which comprise, or alternatively, consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, or 99.9% identical to, for example, any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), or (h), above.

25 The present invention encompasses polypeptide sequences which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, or 99.9% identical to, the following non-limited examples, the polypeptide sequence identified as SEQ ID NO:Y, the polypeptide

30 sequence encoded by a cDNA provided in the deposited clone, and/or polypeptide fragments of any of the polypeptides provided herein. Polynucleotides encoded by these nucleic acid molecules are also encompassed by the invention. In another embodiment, the invention encompasses nucleic acid molecule which comprise, or alternatively, consist of a polynucleotide which hybridizes under stringent conditions,

35 or alternatively, under lower stringency conditions, to a polynucleotide in (a), (b), (c), (d), (e), (f), (g), or (h), above. Polynucleotides which hybridize to the complement of

5 these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polypeptides.

The present invention is also directed to polypeptides which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 10 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, or 99.9% identical to, for example, the polypeptide sequence shown in SEQ ID NO:Y, a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the cDNA in cDNA plasmid:Z, and/or polypeptide fragments of any of these polypeptides (e.g., those 15 fragments described herein). Polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these polypeptides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the present invention, as are the polypeptides encoded by these polynucleotides.

By a nucleic acid having a nucleotide sequence at least, for example, 95% 20 "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% 25 identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence referenced in Table 1, the ORF (open reading frame), or any fragment 30 specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining 35 the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be

5 determined using the CLUSTALW computer program (Thompson, J.D., et al., Nucleic  
Acids Research, 2(22):4673-4680, (1994)), which is based on the algorithm of  
Higgins, D.G., et al., Computer Applications in the Biosciences (CABIOS), 8(2):189-  
191, (1992). In a sequence alignment the query and subject sequences are both DNA  
sequences. An RNA sequence can be compared by converting U's to T's. However,  
10 the CLUSTALW algorithm automatically converts U's to T's when comparing RNA  
sequences to DNA sequences. The result of said global sequence alignment is in  
percent identity. Preferred parameters used in a CLUSTALW alignment of DNA  
sequences to calculate percent identity via pairwise alignments are: Matrix=IUB, k-  
tuple=1, Number of Top Diagonals=5, Gap Penalty=3, Gap Open Penalty 10, Gap  
15 Extension Penalty=0.1, Scoring Method=Percent, Window Size=5 or the length of the  
subject nucleotide sequence, whichever is shorter. For multiple alignments, the  
following CLUSTALW parameters are preferred: Gap Opening Penalty=10; Gap  
Extension Parameter=0.05; Gap Separation Penalty Range=8; End Gap Separation  
Penalty=Off; % Identity for Alignment Delay=40%; Residue Specific Gaps:Off;  
20 Hydrophilic Residue Gap=Off; and Transition Weighting=0. The pairwise and  
multiple alignment parameters provided for CLUSTALW above represent the default  
parameters as provided with the AlignX software program (Vector NTI suite of  
programs, version 6.0).

25 The present invention encompasses the application of a manual correction to  
the percent identity results, in the instance where the subject sequence is shorter than  
the query sequence because of 5' or 3' deletions, not because of internal deletions. If  
only the local pairwise percent identity is required, no manual correction is needed.  
However, a manual correction may be applied to determine the global percent identity  
from a global polynucleotide alignment. Percent identity calculations based upon  
30 global polynucleotide alignments are often preferred since they reflect the percent  
identity between the polynucleotide molecules as a whole (i.e., including any  
polynucleotide overhangs, not just overlapping regions), as opposed to, only local  
matching polynucleotides. Manual corrections for global percent identity  
determinations are required since the CLUSTALW program does not account for 5'  
35 and 3' truncations of the subject sequence when calculating percent identity. For  
subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the

5 percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the CLUSTALW sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above CLUSTALW  
10 program using the specified parameters, to arrive at a final percent identity score. This corrected score may be used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the CLUSTALW alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

15 For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the CLUSTALW alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number  
20 of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the CLUSTALW program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject  
25 sequence which are not matched/aligned with the query. In this case the percent identity calculated by CLUSTALW is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are required for the purposes of the present invention.

30 By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other  
35 words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject

5 sequence may be inserted, deleted, or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

10 As a practical matter, whether any particular polypeptide is at least 80%, 85%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to, for instance, an amino acid sequence referenced in Table 1 (SEQ ID NO:2) or to the amino acid sequence encoded by cDNA contained in a deposited clone, can be determined conventionally using known computer programs. A preferred method for determining  
15 the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the CLUSTALW computer program (Thompson, J.D., et al., Nucleic Acids Research, 2(22):4673-4680, (1994)), which is based on the algorithm of Higgins, D.G., et al., Computer Applications in the Biosciences (CABIOS), 8(2):189-  
20 191, (1992). In a sequence alignment the query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a CLUSTALW alignment of DNA sequences to calculate percent identity via pairwise alignments are: Matrix=BLOSUM, k-tuple=1, Number of Top Diagonals=5, Gap Penalty=3, Gap Open Penalty 10, Gap Extension  
25 Penalty=0.1, Scoring Method=Percent, Window Size=5 or the length of the subject nucleotide sequence, whichever is shorter. For multiple alignments, the following CLUSTALW parameters are preferred: Gap Opening Penalty=10; Gap Extension Parameter=0.05; Gap Separation Penalty Range=8; End Gap Separation Penalty=Off; % Identity for Alignment Delay=40%; Residue Specific Gaps:Off; Hydrophilic  
30 Residue Gap=Off; and Transition Weighting=0. The pairwise and multiple alignment parameters provided for CLUSTALW above represent the default parameters as provided with the AlignX software program (Vector NTI suite of programs, version 6.0).

The present invention encompasses the application of a manual correction to  
35 the percent identity results, in the instance where the subject sequence is shorter than the query sequence because of N- or C-terminal deletions, not because of internal

5 deletions. If only the local pairwise percent identity is required, no manual correction is needed. However, a manual correction may be applied to determine the global percent identity from a global polypeptide alignment. Percent identity calculations based upon global polypeptide alignments are often preferred since they reflect the percent identity between the polypeptide molecules as a whole (i.e., including any 10 polypeptide overhangs, not just overlapping regions), as opposed to, only local matching polypeptides. Manual corrections for global percent identity determinations are required since the CLUSTALW program does not account for N- and C-terminal truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the 15 percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the CLUSTALW sequence alignment. This percentage is then subtracted from the 20 percent identity, calculated by the above CLUSTALW program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what may be used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity 25 score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the CLUSTALW alignment does not 30 show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C-termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the CLUSTALW program. If the remaining 90 residues were perfectly matched the final percent identity would be 35 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no

5 residues at the N- or C-termini of the subject sequence, which are not matched/aligned with the query. In this case the percent identity calculated by CLUSTALW is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the CLUSTALW alignment, which are not matched/aligned with the query sequence are manually corrected for. No other  
10 manual corrections are required for the purposes of the present invention.

In addition to the above method of aligning two or more polynucleotide or polypeptide sequences to arrive at a percent identity value for the aligned sequences, it may be desirable in some circumstances to use a modified version of the CLUSTALW algorithm which takes into account known structural features of the  
15 sequences to be aligned, such as for example, the SWISS-PROT designations for each sequence. The result of such a modified CLUSTALW algorithm may provide a more accurate value of the percent identity for two polynucleotide or polypeptide sequences. Support for such a modified version of CLUSTALW is provided within the CLUSTALW algorithm and would be readily appreciated to one of skill in the art  
20 of bioinformatics.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced  
25 by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the mRNA to those preferred by a bacterial host such as *E. coli*).

30 Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may  
35 be produced by mutagenesis techniques or by direct synthesis.

5 Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the protein without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988 (1993),  
10 reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein (Dobeli et al., *J. Biotechnology* 7:199-216 (1988)).

Moreover, ample evidence demonstrates that variants often retain a biological 15 activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (*J. Biol. Chem.* 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible 20 amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or 25 C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the protein will likely be retained when less than the majority of the residues of the protein are removed from the N-terminus or C-terminus. Whether a particular polypeptide 30 lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Alternatively, such N-terminus or C-terminus deletions of a polypeptide of the present invention may, in fact, result in a significant increase in one or more of the 35 biological activities of the polypeptide(s). For example, biological activity of many polypeptides are governed by the presence of regulatory domains at either one or both

5 termini. Such regulatory domains effectively inhibit the biological activity of such polypeptides in lieu of an activation event (e.g., binding to a cognate ligand or receptor, phosphorylation, proteolytic processing, etc.). Thus, by eliminating the regulatory domain of a polypeptide, the polypeptide may effectively be rendered biologically active in the absence of an activation event.

10 The invention further includes polypeptide variants that show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., *Science* 247:1306-1310  
15 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

20 The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

25 The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, *Science* 244:1081-1085 (1989).) The resulting mutant  
30 molecules can then be tested for biological activity.

35 As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved.

5 The invention encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by the polypeptide of the present invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics (e.g.,  
 10 chemical properties). According to Cunningham et al above, such conservative substitutions are likely to be phenotypically silent. Additional guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie et al., *Science* 247:1306-1310 (1990).

15 Tolerated conservative amino acid substitutions of the present invention involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

20 In addition, the present invention also encompasses the conservative substitutions provided in Table III below.

Table III

For Amino Acid	Code	Replace with any of:
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, $\beta$ -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline
Proline	P	D-Pro, L-1-thiazolidine-4-carboxylic acid, D- or L-1-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

5        Aside from the uses described above, such amino acid substitutions may also increase protein or peptide stability. The invention encompasses amino acid substitutions that contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the protein or peptide sequence. Also included are substitutions that include amino acid residues other than naturally occurring L-amino acids, e.g., D-  
10      amino acids or non-naturally occurring or synthetic amino acids, e.g.,  $\beta$  or  $\gamma$  amino acids.

Both identity and similarity can be readily calculated by reference to the following publications: Computational Molecular Biology, Lesk, A.M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, 15      Smith, D.W., ed., Academic Press, New York, 1993; Informatics Computer Analysis of Sequence Data, Part 1, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991.

20        In addition, the present invention also encompasses substitution of amino acids based upon the probability of an amino acid substitution resulting in conservation of function. Such probabilities are determined by aligning multiple genes with related function and assessing the relative penalty of each substitution to proper gene function. Such probabilities are often described in a matrix and are used 25      by some algorithms (e.g., BLAST, CLUSTALW, GAP, etc.) in calculating percent similarity wherein similarity refers to the degree by which one amino acid may substitute for another amino acid without loss of function. An example of such a matrix is the PAM250 or BLOSUM62 matrix.

30        Aside from the canonical chemically conservative substitutions referenced above, the invention also encompasses substitutions which are typically not classified as conservative, but that may be chemically conservative under certain circumstances. Analysis of enzymatic catalysis for proteases, for example, has shown that certain amino acids within the active site of some enzymes may have highly perturbed pKa's due to the unique microenvironment of the active site. Such perturbed pKa's could 35      enable some amino acids to substitute for other amino acids while conserving enzymatic structure and function. Examples of amino acids that are known to have

5 amino acids with perturbed pKa's are the Glu-35 residue of Lysozyme, the Ile-16 residue of Chymotrypsin, the His-159 residue of Papain, etc. The conservation of function relates to either anomalous protonation or anomalous deprotonation of such amino acids, relative to their canonical, non-perturbed pKa. The pKa perturbation may enable these amino acids to actively participate in general acid-base catalysis due  
10 to the unique ionization environment within the enzyme active site. Thus, substituting an amino acid capable of serving as either a general acid or general base within the microenvironment of an enzyme active site or cavity, as may be the case, in the same or similar capacity as the wild-type amino acid, would effectively serve as a conservative amino substitution.

15 Besides conservative amino acid substitution, variants of the present invention include, but are not limited to, the following: (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature  
20 polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art  
25 from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the  
30 aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Moreover, the invention further includes polypeptide variants created through the application of molecular evolution ("DNA Shuffling") methodology to the  
35 polynucleotide disclosed as SEQ ID NO:X, the sequence of the clone submitted in a deposit, and/or the cDNA encoding the polypeptide disclosed as SEQ ID NO:Y. Such

5 DNA Shuffling technology is known in the art and more particularly described elsewhere herein (e.g., WPC, Stemmer, PNAS, 91:10747, (1994)), and in the Examples provided herein).

10 A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of the present invention having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid substitutions. Of course, in order of ever-increasing preference, it is highly preferable for a peptide or polypeptide 15 to have an amino acid sequence which comprises the amino acid sequence of the present invention, which contains at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 amino acid substitutions. In specific embodiments, the number of additions, substitutions, and/or deletions in the amino acid sequence of the present invention or fragments thereof (e.g., the mature form and/or other fragments described herein), is 20 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, conservative amino acid substitutions are preferable.

#### 4 **Polynucleotide and Polypeptide Fragments**

25 The present invention is directed to polynucleotide fragments of the polynucleotides of the invention, in addition to polypeptides encoded therein by said polynucleotides and/or fragments.

30 In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence which: is a portion of that contained in a deposited clone, or encoding the polypeptide encoded by the cDNA in a deposited clone; is a portion of that shown in SEQ ID NO:X or the complementary strand thereto, or is a portion of a polynucleotide sequence encoding the polypeptide of SEQ ID NO:Y. The nucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, or at least about 150 nt in length. A fragment "at least 20 nt in length," for 35 example, is intended to include 20 or more contiguous bases from the cDNA sequence

5 contained in a deposited clone or the nucleotide sequence shown in SEQ ID NO:X. In this context "about" includes the particularly recited value, a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus, or at both termini. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150,  
10 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750,  
15 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X, or the complementary strand thereto, or the cDNA contained in a deposited clone. In this context "about" includes the particularly recited ranges, and ranges larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein. Also encompassed by the present invention are polynucleotides which  
20 hybridize to these nucleic acid molecules under stringent hybridization conditions or lower stringency conditions, as are the polypeptides encoded by these polynucleotides.

In the present invention, a "polypeptide fragment" refers to an amino acid sequence which is a portion of that contained in SEQ ID NO:Y or encoded by the  
30 cDNA contained in a deposited clone. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90,  
35

5 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, and ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Preferred polypeptide fragments include the full-length protein. Further 10 preferred polypeptide fragments include the full-length protein having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of the full-length polypeptide. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the full-length 15 protein. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and 20 alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are 25 specifically contemplated by the present invention. Moreover, polynucleotides encoding these domains are also contemplated.

Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological 30 activity of the fragments may include an improved desired activity, or a decreased undesirable activity. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

In a preferred embodiment, the functional activity displayed by a polypeptide encoded by a polynucleotide fragment of the invention may be one or more biological 35 activities typically associated with the full-length polypeptide of the invention. Illustrative of these biological activities includes the fragments ability to bind to at

5 least one of the same antibodies which bind to the full-length protein, the fragments ability to interact with at least one of the same proteins which bind to the full-length, the fragments ability to elicit at least one of the same immune responses as the full-length protein (i.e., to cause the immune system to create antibodies specific to the same epitope, etc.), the fragments ability to bind to at least one of the same  
10 polynucleotides as the full-length protein, the fragments ability to bind to a receptor of the full-length protein, the fragments ability to bind to a ligand of the full-length protein, and the fragments ability to multimerize with the full-length protein. However, the skilled artisan would appreciate that some fragments may have biological activities which are desirable and directly inapposite to the biological  
15 activity of the full-length protein. The functional activity of polypeptides of the invention, including fragments, variants, derivatives, and analogs thereof can be determined by numerous methods available to the skilled artisan, some of which are described elsewhere herein.

The present invention encompasses polypeptides comprising, or alternatively  
20 consisting of, an epitope of the polypeptide having an amino acid sequence of SEQ ID NO:Y, or an epitope of the polypeptide sequence encoded by a polynucleotide sequence contained in ATCC deposit No. Z or encoded by a polynucleotide that hybridizes to the complement of the sequence of SEQ ID NO:X or contained in ATCC deposit No. Z under stringent hybridization conditions or lower stringency  
25 hybridization conditions as defined supra. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:1), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize  
30 to the complementary strand under stringent hybridization conditions or lower stringency hybridization conditions defined supra.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a

5 protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described infra. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined  
10 by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross- reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

15 Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985), further described in U.S. Patent No. 4,631,211).

20 In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length, or longer. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof.  
25 Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 37:767-778  
30 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

35 Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides

5 comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to  
10 be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g.,  
15 Sutcliffe et al., *supra*; Wilson et al., *supra*, and Bittle et al., *J. Gen. Virol.*, 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier  
20 using a linker such as maleimidobenzoyl- N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg of peptide or carrier protein and  
25 Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by  
30 selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention comprising an immunogenic or antigenic epitope can be fused to other polypeptide sequences. For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins  
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5 (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of  
10 mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., *Nature*, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked  
15 dimeric structure due to the IgG portion disulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., *J. Biochem.*, 270:3958-3964 (1995). Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA")  
20 tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:8972- 897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of  
25 the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni<sup>2+</sup> nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

30 Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the  
35 polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al., *Curr. Opinion Biotechnol.* 8:724-33

5 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. Biol. 287:265-76 (1999); and Lorenzo and Blasco, Biotechniques 24(2):308- 13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by  
10 DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to  
15 recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

20 *Antibodies*

Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of SEQ ID NO:Y, and/or an epitope, of the present invention (as determined by immunoassays well known in the art for assaying specific antibody-  
25 antigen binding). Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, monovalent, bispecific, heteroconjugate, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention),  
30 and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2,  
35 IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule. Moreover, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact

5 molecules, as well as, antibody fragments (such as, for example, Fab and F(ab')2 fragments) which are capable of specifically binding to protein. Fab and F(ab')2 fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation of the animal or plant, and may have less non-specific tissue binding than an intact antibody (Wahl et al., J. Nucl. Med. 24:316-325 (1983)). Thus, these  
10 fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')2, Fd, 15 single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding 20 fragments also comprising any combination of variable region(s) with a hinge region, CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, sheep rabbit, goat, guinea pig, camel, horse, or chicken. As used herein, "human" antibodies include antibodies having the amino 25 acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described infra and, for example in, U.S. Patent No. 5,939,598 by Kucherlapati et al.

The antibodies of the present invention may be monospecific, bispecific, 30 trispecific or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol. 35 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

5       Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, by size in contiguous amino acid residues, or listed in the Tables and Figures. Antibodies which  
10 specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that specifically bind polypeptides of the present invention, and allows for the exclusion of the same.

Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog, or homologue of a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react with murine, rat and/or rabbit homologues of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under stringent hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or Kd less than 5 X 10-2 M, 10-2 M, 5 X 10-3 M, 10-3 M, 5 X 10-4 M, 10-4 M, 5 X 10-5 M, 10-5 M, 5 X 10-6 M, 10-6 M, 5 X 10-7 M, 107 M, 5 X 10-8 M, 10-8 M, 5 X 10-9 M, 10-9 M, 5 X 10-10 M.

5 M, 10-10 M, 5 X 10-11 M, 10-11 M, 5 X 10-12 M, 10-12 M, 5 X 10-13 M, 10-13 M,  
5 X 10-14 M, 10-14 M, 5 X 10-15 M, or 10-15 M.

The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described 10 herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at least 95%, at least 90%, at least 85 %, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes 15 antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferably, antibodies of the present invention bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent 20 receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described *supra*). In specific embodiments, 25 antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.

The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the 30 receptor-ligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention 35 are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of

5 the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Patent No. 10 5,811,097; Deng et al., Blood 92(6):1981-1988 (1998); Chen et al., Cancer Res. 58(16):3668-3678 (1998); Harrop et al., J. Immunol. 161(4):1786-1794 (1998); Zhu et al., Cancer Res. 58(15):3209-3214 (1998); Yoon et al., J. Immunol. 160(7):3170-3179 (1998); Prat et al., J. Cell. Sci. 111(Pt2):237-247 (1998); Pitard et al., J. Immunol. Methods 205(2):177-190 (1997); Liautard et al., Cytokine 9(4):233-241 (1997); 15 Carlson et al., J. Biol. Chem. 272(17):11295-11301 (1997); Taryman et al., Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9):1153-1167 (1998); Bartunek et al., Cytokine 8(1):14-20 (1996) (which are all incorporated by reference herein in their entireties).

Antibodies of the present invention may be used, for example, but not limited 20 to, to purify, detect, and target the polypeptides of the present invention, including both in vitro and in vivo diagnostic and therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory 25 Press, 2nd ed. 1988) (incorporated by reference herein in its entirety).

As discussed in more detail below, the antibodies of the present invention may be used either alone or in combination with other compositions. The antibodies may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus 30 or chemically conjugated (including covalently and non-covalently conjugations) to polypeptides or other compositions. For example, antibodies of the present invention may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, radionucleotides, or toxins. See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Patent No. 5,314,995; and EP 396,387.

35 The antibodies of the invention include derivatives that are modified, i.e., by the covalent attachment of any type of molecule to the antibody such that covalent

5 attachment does not prevent the antibody from generating an anti-idiotypic response. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of  
10 numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more non-classical amino acids.

15 The antibodies of the present invention may be generated by any suitable method known in the art.

The antibodies of the present invention may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan (Harlow, et al., *Antibodies: A Laboratory Manual*, (Cold spring Harbor Laboratory Press, 2<sup>nd</sup> ed. (1988), which is hereby incorporated herein by reference in its entirety). For  
20 example, a polypeptide of the invention can be administered to various host animals including, but not limited to, rabbits, mice, rats, etc. to induce the production of sera containing polyclonal antibodies specific for the antigen. The administration of the polypeptides of the present invention may entail one or more injections of an immunizing agent and, if desired, an adjuvant. Various adjuvants may be used to  
25 increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and  
30 corynebacterium parvum. Such adjuvants are also well known in the art. For the purposes of the invention, "immunizing agent" may be defined as a polypeptide of the invention, including fragments, variants, and/or derivatives thereof, in addition to fusions with heterologous polypeptides and other forms of the polypeptides described herein.

35 Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections, though they may also

5 be given intramuscularly, and/or through IV). The immunizing agent may include polypeptides of the present invention or a fusion protein or variants thereof. Depending upon the nature of the polypeptides (i.e., percent hydrophobicity, percent hydrophilicity, stability, net charge, isoelectric point etc.), it may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the  
10 mammal being immunized. Such conjugation includes either chemical conjugation by derivitizing active chemical functional groups to both the polypeptide of the present invention and the immunogenic protein such that a covalent bond is formed, or through fusion-protein based methodology, or other methods known to the skilled artisan. Examples of such immunogenic proteins include, but are not limited to  
15 keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions,  
20 keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and Corynebacterium parvum. Additional examples of adjuvants which may be employed includes the MPL-TDM adjuvant (monophosphoryl lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

25 The antibodies of the present invention may comprise monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975) and U.S. Pat. No. 4,376,110, by Harlow, et al., *Antibodies: A Laboratory Manual*, (Cold spring Harbor Laboratory Press, 2<sup>nd</sup> ed. (1988), by Hammerling, et al., *Monoclonal Antibodies and T-Cell Hybridomas* (Elsevier, N.Y., (1981)), or other methods known to the artisan.  
30 Other examples of methods which may be employed for producing monoclonal antibodies includes, but are not limited to, the human B-cell hybridoma technique (Kosbor et al., 1983, *Immunology Today* 4:72; Cole et al., 1983, *Proc. Natl. Acad. Sci. USA* 80:2026-2030), and the EBV-hybridoma technique (Cole et al., 1985, *Monoclonal Antibodies And Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD

5 and any subclass thereof. The hybridoma producing the mAb of this invention may be cultivated in vitro or in vivo. Production of high titers of mAbs in vivo makes this the presently preferred method of production.

In a hybridoma method, a mouse, a humanized mouse, a mouse with a human immune system, hamster, or other appropriate host animal, is typically immunized 10 with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro.

The immunizing agent will typically include polypeptides of the present invention or a fusion protein thereof. Generally, either peripheral blood lymphocytes 15 ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986), pp. 59-103). Immortalized cell lines 20 are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine 25 guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable 30 high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. As inferred throughout the specification, human myeloma and mouse-human heteromyeloma cell lines also have been described for 35 the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001

5 (1984); Brodeur et al., *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the polypeptides of the present invention. Preferably, the binding specificity of monoclonal antibodies 10 produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbant assay (ELISA). Such techniques are known in the art and within the skill of the artisan. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollart, *Anal. 15 Biochem.*, 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, *supra*). Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640. Alternatively, the hybridoma cells may be grown in 20 *vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-sepharose, hydroxyapatite chromatography, gel exclusion chromatography, gel electrophoresis, dialysis, or 25 affinity chromatography.

The skilled artisan would acknowledge that a variety of methods exist in the art for the production of monoclonal antibodies and thus, the invention is not limited to their sole production in hydridomas. For example, the monoclonal antibodies may be made by recombinant DNA methods, such as those described in US patent No. 4, 30 816, 567. In this context, the term "monoclonal antibody" refers to an antibody derived from a single eukaryotic, phage, or prokaryotic clone. The DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine 35 antibodies, or such chains from human, humanized, or other sources). The hydridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the

5 DNA may be placed into expression vectors, which are then transformed into host cells such as Simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain  
10 constant domains in place of the homologous murine sequences (US Patent No. 4, 816, 567; Morrison et al, *supra*) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the  
15 variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain.  
20 The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can  
25 be accomplished using routine techniques known in the art. Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., *Antibodies:*  
30 A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an  
35 antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

5        Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art and are discussed in detail in the Examples described herein. In a non-limiting example, mice can be immunized with a polypeptide of the invention or a cell expressing such peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse  
10      serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP20 available from the ATCC. Hybridomas are selected and cloned by limited dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention.  
15      Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

Accordingly, the present invention provides methods of generating monoclonal antibodies as well as antibodies produced by the method comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably,  
20      the hybridoma is generated by fusing splenocytes isolated from a mouse immunized with an antigen of the invention with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind a polypeptide of the invention.

Antibody fragments which recognize specific epitopes may be generated by  
25      known techniques. For example, Fab and F(ab')2 fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). F(ab')2 fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

30      For example, the antibodies of the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains expressed from a repertoire  
35      or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified

5 with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make  
10 the antibodies of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods 182:41-50 (1995); Ames et al., J. Immunol. Methods 184:177-186 (1995); Kettleborough et al., Eur. J. Immunol. 24:952-958 (1994); Persic et al., Gene 187 9-18 (1997); Burton et al., Advances in Immunology 57:191-280 (1994); PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737;  
15 WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody  
20 coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')2 fragments can also be employed using  
25 methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., BioTechniques 12(6):864-869 (1992); and Sawai et al., AJRI 34:26-34 (1995); and Better et al., Science 240:1041-1043 (1988) (said references incorporated by reference in their entireties). Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S.  
30 Patents 4,946,778 and 5,258,498; Huston et al., Methods in Enzymology 203:46-88 (1991); Shu et al., PNAS 90:7995-7999 (1993); and Skerra et al., Science 240:1038-1040 (1988).

For some uses, including in vivo use of antibodies in humans and in vitro  
35 detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a

5 variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Gillies et al., (1989) *J. Immunol. Methods* 125:191-202; U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein  
10 by reference in their entirety. Humanized antibodies are antibody molecules from non-human species antibody that binds the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and a framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding  
15 residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al.,  
20 U.S. Patent No. 5,585,089; Riechmann et al., *Nature* 332:323 (1988), which are incorporated herein by reference in their entireties.) Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Patent Nos. 5,225,539; 5,530,101; and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Padlan, *Molecular  
25 Immunology* 28(4/5):489-498 (1991); Studnicka et al., *Protein Engineering* 7(6):805-814 (1994); Roguska. et al., *PNAS* 91:969-973 (1994)), and chain shuffling (U.S. Patent No. 5,565,332). Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from  
30 an "import" variable domain. Humanization can be essentially performed following the methods of Winter and co-workers (Jones et al., *Nature*, 321:522-525 (1986); Reichmann et al., *Nature*, 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are  
35 chimeric antibodies (US Patent No. 4, 816, 567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence

5 from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted from analogous sites in rodent antibodies.

In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR 10 regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature* 332:323-329 15 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)).

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody libraries derived from human immunoglobulin sequences. See also, U.S. Patent Nos. 20 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety. The techniques of Cole et al., and Boerder et al., are also available for the preparation of human monoclonal antibodies (cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Riss, 25 (1985); and Boerner et al., *J. Immunol.*, 147(1):86-95, (1991)).

Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes may be introduced randomly or by homologous 30 recombination into mouse embryonic stem cells. Alternatively, the human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes may be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous 35 recombination. In particular, homozygous deletion of the JH region prevents endogenous antibody production. The modified embryonic stem cells are expanded

5 and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained from the immunized, transgenic mice using conventional  
10 hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, *Int. Rev.*  
15 *Immunol.* 13:65-93 (1995). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent No. 0 598 877; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793;  
20 5,916,771; and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Freemont, CA), Genpharm (San Jose, CA), and Medarex, Inc. (Princeton, NJ) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Similarly, human antibodies can be made by introducing human  
25 immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and creation of an antibody repertoire. This approach is described, for example, in US patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,106, and in the following scientific publications: Marks et al., *Biotechnol.*, 10:779-783 (1992); Lonberg et al., *Nature* 368:856-859 (1994); Fishwild et al., *Nature Biotechnol.*, 14:845-51 (1996); Neuberger, *Nature Biotechnol.*, 14:826 (1996); Lonberg and Huszer, *Intern. Rev. Immunol.*, 13:65-93 (1995).

35 Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a

5 selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., Bio/technology 12:899-903 (1988)).

Further, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotype antibodies that "mimic" polypeptides of the invention using 10 techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, FASEB J. 7(5):437-444; (1989) and Nissinoff, J. Immunol. 147(8):2429-2438 (1991)). For example, antibodies which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to a ligand can be used to generate anti-idiotypes that "mimic" the polypeptide multimerization and/or 15 binding domain and, as a consequence, bind to and neutralize polypeptide and/or its ligand. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize polypeptide ligand. For example, such anti-idiotypic antibodies can be used to bind a polypeptide of the invention and/or to bind its ligands/receptors, and thereby block its biological activity.

20 The antibodies of the present invention may be bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present invention, one of the binding specificities may be directed towards a polypeptide of the present invention, the other may be for any other antigen, and preferably for a cell-surface 25 protein, receptor, receptor subunit, tissue-specific antigen, virally derived protein, virally encoded envelope protein, bacterially derived protein, or bacterial surface protein, etc.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of 30 two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct 35 molecule is usually accomplished by affinity chromatography steps. Similar

5 procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, 10 comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transformed into a suitable 15 host organism. For further details of generating bispecific antibodies see, for example Suresh et al., Meth. In Enzym., 121:210 (1986).

Heteroconjugate antibodies are also contemplated by the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to 20 unwanted cells (US Patent No. 4, 676, 980), and for the treatment of HIV infection (WO 91/00360; WO 92/20373; and EP03089). It is contemplated that the antibodies may be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioester bond. 25 Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in US Patent No. 4,676,980.

#### *Polynucleotides Encoding Antibodies*

The invention further provides polynucleotides comprising a nucleotide sequence encoding an antibody of the invention and fragments thereof. The invention 30 also encompasses polynucleotides that hybridize under stringent or lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, that specifically binds to a polypeptide of the invention, preferably, an antibody that binds to a polypeptide having the amino acid sequence of 35 SEQ ID NO:Y.

The polynucleotides may be obtained, and the nucleotide sequence of the

5 polynucleotides determined, by any method known in the art. For example, if the nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody may be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., BioTechniques 17:242 (1994)), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the  
10 antibody, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is  
15 known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable to the 3'  
20 and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence and corresponding amino acid sequence of the  
25 antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY  
30 and Ausubel et al., eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY, which are both incorporated by reference herein in their entireties ), to generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

In a specific embodiment, the amino acid sequence of the heavy and/or light  
35 chain variable domains may be inspected to identify the sequences of the complementarity determining regions (CDRs) by methods that are well known in the

5 art, e.g., by comparison to known amino acid sequences of other heavy and light chain variable regions to determine the regions of sequence hypervariability. Using routine recombinant DNA techniques, one or more of the CDRs may be inserted within framework regions, e.g., into human framework regions to humanize a non-human antibody, as described supra. The framework regions may be naturally occurring or  
10 consensus framework regions, and preferably human framework regions (see, e.g., Chothia et al., J. Mol. Biol. 278: 457-479 (1998) for a listing of human framework regions). Preferably, the polynucleotide generated by the combination of the framework regions and CDRs encodes an antibody that specifically binds a polypeptide of the invention. Preferably, as discussed supra, one or more amino acid  
15 substitutions may be made within the framework regions, and, preferably, the amino acid substitutions improve binding of the antibody to its antigen. Additionally, such methods may be used to make amino acid substitutions or deletions of one or more variable region cysteine residues participating in an intrachain disulfide bond to generate antibody molecules lacking one or more intrachain disulfide bonds. Other  
20 alterations to the polynucleotide are encompassed by the present invention and within the skill of the art.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., Proc. Natl. Acad. Sci. 81:851-855 (1984); Neuberger et al., Nature 312:604-608 (1984); Takeda et al., Nature 314:452-454 (1985)) by splicing genes 25 from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region, e.g., humanized  
30 antibodies.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778; Bird, Science 242:423- 42 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature 334:544-54 (1989)) can be adapted to produce single chain antibodies. Single chain 35 antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the

5 assembly of functional Fv fragments in *E. coli* may also be used (Skerra et al.,  
10 *Science* 242:1038- 1041 (1988)).

*Methods of Producing Antibodies*

The antibodies of the invention can be produced by any method known in the  
10 art for the synthesis of antibodies, in particular, by chemical synthesis or preferably,  
by recombinant expression techniques.

Recombinant expression of an antibody of the invention, or fragment,  
derivative or analog thereof, (e.g., a heavy or light chain of an antibody of the  
invention or a single chain antibody of the invention), requires construction of an  
15 expression vector containing a polynucleotide that encodes the antibody. Once a  
polynucleotide encoding an antibody molecule or a heavy or light chain of an  
antibody, or portion thereof (preferably containing the heavy or light chain variable  
domain), of the invention has been obtained, the vector for the production of the  
antibody molecule may be produced by recombinant DNA technology using  
20 techniques well known in the art. Thus, methods for preparing a protein by expressing  
a polynucleotide containing an antibody encoding nucleotide sequence are described  
herein. Methods which are well known to those skilled in the art can be used to  
construct expression vectors containing antibody coding sequences and appropriate  
transcriptional and translational control signals. These methods include, for example,  
25 in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic  
recombination. The invention, thus, provides replicable vectors comprising a  
nucleotide sequence encoding an antibody molecule of the invention, or a heavy or  
light chain thereof, or a heavy or light chain variable domain, operably linked to a  
promoter. Such vectors may include the nucleotide sequence encoding the constant  
30 region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT  
Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of  
the antibody may be cloned into such a vector for expression of the entire heavy or  
light chain.

The expression vector is transferred to a host cell by conventional techniques  
35 and the transfected cells are then cultured by conventional techniques to produce an  
antibody of the invention. Thus, the invention includes host cells containing a

5 polynucleotide encoding an antibody of the invention, or a heavy or light chain thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the expression of double-chained antibodies, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

10 A variety of host-expression vector systems may be utilized to express the antibody molecules of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody molecule of the 15 invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant 20 virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) 25 harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *Escherichia coli*, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used 30 for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., Gene 45:101 (1986); Cockett et al., Bio/Technology 8:2 (1990)).

35 In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the antibody molecule being expressed.

5 For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., EMBO J. 2:1791 (1983)), in which the antibody coding  
10 sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, Nucleic Acids Res. 13:3101-3109 (1985); Van Heeke & Schuster, J. Biol. Chem.. 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such  
15 fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

20 In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

25 In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the antibody coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo  
30 recombination. Insertion in a non- essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (e.g., see Logan & Shenk, Proc. Natl. Acad. Sci. USA 81:355-359 (1984)). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the  
35 ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure

5 translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., Methods in Enzymol. 153:51-544 (1987)).

10 In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-  
15 translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such  
20 mammalian host cells include but are not limited to CHO, VERY, BHK, Hela, COS, MDCK, 293, 3T3, WI38, and in particular, breast cancer cell lines such as, for example, BT483, Hs578T, HTB2, BT20 and T47D, and normal mammary gland cell line such as, for example, CRL7030 and Hs578Bst.

For long-term, high-yield production of recombinant proteins, stable  
25 expression is preferred. For example, cell lines which stably express the antibody molecule may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker.  
30 Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may  
35 advantageously be used to engineer cell lines which express the antibody molecule. Such engineered cell lines may be particularly useful in screening and evaluation of

5 compounds that interact directly or indirectly with the antibody molecule.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., *Cell* 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, *Proc. Natl. Acad. Sci. USA* 48:202 (1992)), and adenine phosphoribosyltransferase (Lowy et al., *Cell* 22:817 (1980)) genes can be employed in tk-, hgprt- or aprt- cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., *Natl. Acad. Sci. USA* 77:357 (1980); O'Hare et al., *Proc. Natl. Acad. Sci. USA* 78:1527 (1981)); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, *Proc. Natl. Acad. Sci. USA* 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-418 *Clinical Pharmacy* 12:488-505; Wu and Wu, *Biotherapy* 3:87-95 (1991); Tolstoshev, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596 (1993); Mulligan, *Science* 260:926-932 (1993); and Morgan and Anderson, *Ann. Rev. Biochem.* 62:191-217 (1993); May, 1993, *TIB TECH* 11(5):155-215); and hygro, which confers resistance 20 to hygromycin (Santerre et al., *Gene* 30:147 (1984)). Methods commonly known in the art of recombinant DNA technology may be routinely applied to select the desired recombinant clone, and such methods are described, for example, in Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, NY (1993); Kriegler, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY 25 (1990); and in Chapters 12 and 13, Dracopoli et al. (eds), *Current Protocols in Human Genetics*, John Wiley & Sons, NY (1994); Colberre-Garapin et al., *J. Mol. Biol.* 150:1 (1981), which are incorporated by reference herein in their entireties.

The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, *The use of vectors based 30 on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning, Vol.3.* (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will 35 also increase (Crouse et al., *Mol. Cell. Biol.* 3:257 (1983)).

The host cell may be co-transfected with two expression vectors of the

5 invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the  
10 light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, *Nature* 322:52 (1986); Kohler, *Proc. Natl. Acad. Sci. USA* 77:2197 (1980)). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once an antibody molecule of the invention has been produced by an animal, chemically synthesized, or recombinantly expressed, it may be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the 20 purification of proteins. In addition, the antibodies of the present invention or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art, to facilitate purification.

The present invention encompasses antibodies recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugations) to 25 a polypeptide (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention to generate fusion proteins. The fusion does not necessarily need to be direct, but may occur through linker sequences. The antibodies may be specific for antigens other than polypeptides (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino 30 acids of the polypeptide) of the present invention. For example, antibodies may be used to target the polypeptides of the present invention to particular cell types, either in vitro or in vivo, by fusing or conjugating the polypeptides of the present invention to antibodies specific for particular cell surface receptors. Antibodies fused or conjugated to the polypeptides of the present invention may also be used in in vitro 35 immunoassays and purification methods using methods known in the art. See e.g., Harbor et al., *supra*, and PCT publication WO 93/21232; EP 439,095; Naramura et al.,

5 Immunol. Lett. 39:91-99 (1994); U.S. Patent 5,474,981; Gillies et al., PNAS 89:1428-1432 (1992); Fell et al., J. Immunol. 146:2446-2452(1991), which are incorporated by reference in their entireties.

The present invention further includes compositions comprising the polypeptides of the present invention fused or conjugated to antibody domains other than the variable regions. For example, the polypeptides of the present invention may be fused or conjugated to an antibody Fc region, or portion thereof. The antibody portion fused to a polypeptide of the present invention may comprise the constant region, hinge region, CH1 domain, CH2 domain, and CH3 domain or any combination of whole domains or portions thereof. The polypeptides may also be fused or conjugated to the above antibody portions to form multimers. For example, Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present invention to antibody portions are known in the art. See, e.g., U.S. Patent Nos. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 5,447,851; 5,112,946; EP 307,434; EP 367,166; PCT publications WO 96/04388; WO 91/06570; Ashkenazi et al., Proc. Natl. Acad. Sci. USA 88:10535-10539 (1991); Zheng et al., J. Immunol. 154:5590-5600 (1995); and Vil et al., Proc. Natl. Acad. Sci. USA 89:11337- 11341(1992) (said references incorporated by reference in their entireties).

As discussed, *supra*, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of SEQ ID NO:Y may be fused or conjugated to the above antibody portions to increase the *in vivo* half life of the polypeptides or for use in immunoassays using methods known in the art. Further, the polypeptides corresponding to SEQ ID NO:Y may be fused or conjugated to the above antibody portions to facilitate purification. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP 394,827; Traunecker et al., Nature 331:84-86 (1988). The polypeptides of the present invention fused or conjugated to an antibody having disulfide-linked dimeric structures (due to the IgG) may also be more efficient in

5 binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995)). In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP A 232,262). Alternatively, deleting the Fc part after the fusion protein has been  
10 expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, Bennett et al., J. Molecular Recognition 8:52-58  
15 (1995); Johanson et al., J. Biol. Chem.. 270:9459-9471 (1995)).

Moreover, the antibodies or fragments thereof of the present invention can be fused to marker sequences, such as a peptide to facilitate purification. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 20 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson 25 et al., Cell 37:767 (1984)) and the "flag" tag.

The present invention further encompasses antibodies or fragments thereof conjugated to a diagnostic or therapeutic agent. The antibodies can be used diagnostically to, for example, monitor the development or progression of a tumor as part of a clinical testing procedure to, e.g., determine the efficacy of a given treatment 30 regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance 35 may be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art)

5 using techniques known in the art. See, for example, U.S. Patent No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of 10 suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include 125I, 131I, 111In or 99Tc.

15 Further, an antibody or fragment thereof may be conjugated to a therapeutic moiety such as a cytotoxin, e.g., a cytostatic or cytocidal agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, 213Bi. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include paclitaxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, 20 etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologues thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, 25 cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly 30 actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the therapeutic agent or drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a

5    protein such as tumor necrosis factor,  $\alpha$ -interferon,  $\beta$ -interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator, an apoptotic agent, e.g., TNF-alpha, TNF-beta, AIM I (See, International Publication No. WO 97/33899), AIM II (See, International Publication No. WO 97/34911), Fas Ligand (Takahashi et al., Int. Immunol., 6:1567-1574 (1994)), VEGI (See, International Publication No. 10 WO 99/23105), a thrombotic agent or an anti- angiogenic agent, e.g., angiostatin or endostatin; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

15    Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

Techniques for conjugating such therapeutic moiety to antibodies are well 20 known, see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents 25 In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And 30 Cytotoxic Properties Of Antibody-Toxin Conjugates", Immunol. Rev. 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980, which is incorporated herein by reference in its entirety.

35    An antibody, with or without a therapeutic moiety conjugated to it, administered alone or in combination with cytotoxic factor(s) and/or cytokine(s) can

5 be used as a therapeutic.

The present invention also encompasses the creation of synthetic antibodies directed against the polypeptides of the present invention. One example of synthetic antibodies is described in Radrizzani, M., et al., Medicina, (Aires), 59(6):753-8, (1999)). Recently, a new class of synthetic antibodies has been described and are 10 referred to as molecularly imprinted polymers (MIPs) (Semorex, Inc.). Antibodies, peptides, and enzymes are often used as molecular recognition elements in chemical and biological sensors. However, their lack of stability and signal transduction mechanisms limits their use as sensing devices. Molecularly imprinted polymers (MIPs) are capable of mimicking the function of biological receptors but with less 15 stability constraints. Such polymers provide high sensitivity and selectivity while maintaining excellent thermal and mechanical stability. MIPs have the ability to bind to small molecules and to target molecules such as organics and proteins' with equal or greater potency than that of natural antibodies. These "super" MIPs have higher affinities for their target and thus require lower concentrations for efficacious binding.

20 During synthesis, the MIPs are imprinted so as to have complementary size, shape, charge and functional groups of the selected target by using the target molecule itself (such as a polypeptide, antibody, etc.), or a substance having a very similar structure, as its "print" or "template." MIPs can be derivitized with the same reagents afforded to antibodies. For example, fluorescent 'super' MIPs can be coated onto 25 beads or wells for use in highly sensitive separations or assays, or for use in high throughput screening of proteins.

Moreover, MIPs based upon the structure of the polypeptide(s) of the present invention may be useful in screening for compounds that bind to the polypeptide(s) of the invention. Such a MIP would serve the role of a synthetic "receptor" by 30 mimicking the native architecture of the polypeptide. In fact, the ability of a MIP to serve the role of a synthetic receptor has already been demonstrated for the estrogen receptor (Ye, L., Yu, Y., Mosbach, K, Analyst., 126(6):760-5, (2001); Dickert, F, L., Hayden, O., Halikias, K, P, Analyst., 126(6):766-71, (2001)). A synthetic receptor may either be mimicked in its entirety (e.g., as the entire protein), or mimicked as a 35 series of short peptides corresponding to the protein (Rachkov, A., Minoura, N, Biochim, Biophys, Acta., 1544(1-2):255-66, (2001)). Such a synthetic receptor MIPs

5 may be employed in any one or more of the screening methods described elsewhere herein.

MIPs have also been shown to be useful in "sensing" the presence of its mimicked molecule (Cheng, Z., Wang, E., Yang, X, Biosens, Bioelectron., 16(3):179-85, (2001) ; Jenkins, A, L., Yin, R., Jensen, J. L, Analyst., 126(6):798-802, (2001) ; 10 Jenkins, A, L., Yin, R., Jensen, J. L, Analyst., 126(6):798-802, (2001)). For example, a MIP designed using a polypeptide of the present invention may be used in assays designed to identify, and potentially quantitate, the level of said polypeptide in a sample. Such a MIP may be used as a substitute for any component described in the assays, or kits, provided herein (e.g., ELISA, etc.).

15 A number of methods may be employed to create MIPs to a specific receptor, ligand, polypeptide, peptide, or organic molecule. Several preferred methods are described by Esteban et al in J. Anal, Chem., 370(7):795-802, (2001), which is hereby incorporated herein by reference in its entirety in addition to any references cited therein. Additional methods are known in the art and are encompassed by the present 20 invention, such as for example, Hart, B, R., Shea, K, J. J. Am. Chem, Soc., 123(9):2072-3, (2001); and Quaglia, M., Chenon, K., Hall, A, J., De, Lorenzi, E., Sellergren, B, J. Am. Chem, Soc., 123(10):2146-54, (2001); which are hereby incorporated by reference in their entirety herein.

25 **Uses for Antibodies directed against polypeptides of the invention**

The antibodies of the present invention have various utilities. For example, such antibodies may be used in diagnostic assays to detect the presence or quantification of the polypeptides of the invention in a sample. Such a diagnostic assay may be comprised of at least two steps. The first, subjecting a sample with the 30 antibody, wherein the sample is a tissue (e.g., human, animal, etc.), biological fluid (e.g., blood, urine, sputum, semen, amniotic fluid, saliva, etc.), biological extract (e.g., tissue or cellular homogenate, etc.), a protein microchip (e.g., See Arenkov P, et al., Anal Biochem., 278(2):123-131 (2000)), or a chromatography column, etc. And a second step involving the quantification of antibody bound to the substrate. 35 Alternatively, the method may additionally involve a first step of attaching the antibody, either covalently, electrostatically, or reversibly, to a solid support, and a

5 second step of subjecting the bound antibody to the sample, as defined above and elsewhere herein.

Various diagnostic assay techniques are known in the art, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogenous phases (Zola, Monoclonal 10 Antibodies: A Manual of Techniques, CRC Press, Inc., (1987), pp147-158). The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as 2H, 14C, 32P, or 125I, a fluorescent or chemiluminescent compound, such as 15 fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase, green fluorescent protein, or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); Dafvid et al., *Biochem.*, 13:1014 (1974); Pain et al., *J. Immunol. 20 Metho.*, 40:219(1981); and Nygren, *J. Histochem. And Cytochem.*, 30:407 (1982).

Antibodies directed against the polypeptides of the present invention are useful for the affinity purification of such polypeptides from recombinant cell culture or natural sources. In this process, the antibodies against a particular polypeptide are immobilized on a suitable support, such as a Sephadex resin or filter paper, using 25 methods well known in the art. The immobilized antibody then is contacted with a sample containing the polypeptides to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except for the desired polypeptides, which are bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release 30 the desired polypeptide from the antibody.

#### *Immunophenotyping*

The antibodies of the invention may be utilized for immunophenotyping of cell lines and biological samples. The translation product of the gene of the present 35 invention may be useful as a cell specific marker, or more specifically as a cellular marker that is differentially expressed at various stages of differentiation and/or

5 maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, will allow for the screening of cellular populations expressing the marker. Various techniques can be utilized using monoclonal antibodies to screen for cellular populations expressing the marker(s), and include magnetic separation using antibody-coated magnetic beads, "panning" with  
10 antibody attached to a solid matrix (i.e., plate), and flow cytometry (See, e.g., U.S. Patent 5,985,660; and Morrison et al., *Cell*, 96:737-49 (1999)).

These techniques allow for the screening of particular populations of cells, such as might be found with hematological malignancies (i.e. minimal residual disease (MRD) in acute leukemic patients) and "non-self" cells in transplantations to  
15 prevent Graft-versus-Host Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might be found in human umbilical cord blood.

#### *Assays For Antibody Binding*

20 The antibodies of the invention may be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions,  
25 gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known in the art (see, e.g., Ausubel et al, eds, 1994, *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by reference  
30 herein in its entirety). Exemplary immunoassays are described briefly below (but are not intended by way of limitation).

35 Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X- 100, 1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1% Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSF, aprotinin, sodium vanadate), adding the antibody of interest to the cell

5 lysate, incubating for a period of time (e.g., 1-4 hours) at 4° C, adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4° C, washing the beads in lysis buffer and resuspending the beads in SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, e.g., western blot analysis. One of skill in the art  
10 would be knowledgeable as to the parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding immunoprecipitation protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.16.1.

15 Western blot analysis generally comprises preparing protein samples, electrophoresis of the protein samples in a polyacrylamide gel (e.g., 8%- 20% SDS-PAGE depending on the molecular weight of the antigen), transferring the protein sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e.g., PBS with 3% BSA or non-  
20 fat milk), washing the membrane in washing buffer (e.g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer, washing the membrane in washing buffer, blocking the membrane with a secondary antibody (which recognizes the primary antibody, e.g., an anti-human antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or  
25 alkaline phosphatase) or radioactive molecule (e.g., <sup>32</sup>P or <sup>125</sup>I) diluted in blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding western blot protocols see, e.g., Ausubel et al, eds, 1994,  
30 Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.8.1.

ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be  
35

5     conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. One of  
10    skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected as well as other variations of ELISAs known in the art. For further discussion regarding ELISAs see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 11.2.1.

15     The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g.,  $^3\text{H}$  or  $^{125}\text{I}$ ) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the  
20    antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e.g.,  $^3\text{H}$  or  $^{125}\text{I}$ ) in the presence of  
25    increasing amounts of an unlabeled second antibody.

#### *Therapeutic Uses Of Antibodies*

The present invention is further directed to antibody-based therapies which involve administering antibodies of the invention to an animal, preferably a mammal,  
30    and most preferably a human, patient for treating one or more of the disclosed diseases, disorders, or conditions. Therapeutic compounds of the invention include, but are not limited to, antibodies of the invention (including fragments, analogs and derivatives thereof as described herein) and nucleic acids encoding antibodies of the invention (including fragments, analogs and derivatives thereof and anti-idiotypic  
35    antibodies as described herein). The antibodies of the invention can be used to treat, inhibit or prevent diseases, disorders or conditions associated with aberrant expression

5 and/or activity of a polypeptide of the invention, including, but not limited to, any one or more of the diseases, disorders, or conditions described herein. The treatment and/or prevention of diseases, disorders, or conditions associated with aberrant expression and/or activity of a polypeptide of the invention includes, but is not limited to, alleviating symptoms associated with those diseases, disorders or conditions.

10 Antibodies of the invention may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the 15 antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

20 The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors (such as, e.g., IL-2, IL-3 and IL-7), for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

25 The antibodies of the invention may be administered alone or in combination with other types of treatments (e.g., radiation therapy, chemotherapy, hormonal therapy, immunotherapy and anti-tumor agents). Generally, administration of products of a species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, 30 human antibodies, fragments derivatives, analogs, or nucleic acids, are administered to a human patient for therapy or prophylaxis.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and 35 therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will

5 preferably have an affinity for polynucleotides or polypeptides of the invention, including fragments thereof. Preferred binding affinities include those with a dissociation constant or  $K_d$  less than  $5 \times 10^{-2}$  M,  $10^{-2}$  M,  $5 \times 10^{-3}$  M,  $10^{-3}$  M,  $5 \times 10^{-4}$  M,  $10^{-4}$  M,  $5 \times 10^{-5}$  M,  $10^{-5}$  M,  $5 \times 10^{-6}$  M,  $10^{-6}$  M,  $5 \times 10^{-7}$  M,  $10^{-7}$  M,  $5 \times 10^{-8}$  M,  $10^{-8}$  M,  $5 \times 10^{-9}$  M,  $10^{-9}$  M,  $5 \times 10^{-10}$  M,  $10^{-10}$  M,  $5 \times 10^{-11}$  M,  $10^{-11}$  M,  $5 \times 10^{-12}$  M,  $10^{-12}$  M,  $5 \times 10^{-13}$  M,  $10^{-13}$  M,  $5 \times 10^{-14}$  M,  $10^{-14}$  M,  $5 \times 10^{-15}$  M, and  $10^{-15}$  M.

10 Antibodies directed against polypeptides of the present invention are useful for inhibiting allergic reactions in animals. For example, by administering a therapeutically acceptable dose of an antibody, or antibodies, of the present invention, or a cocktail of the present antibodies, or in combination with other antibodies of varying sources, the animal may not elicit an allergic response to antigens.

15 Likewise, one could envision cloning the gene encoding an antibody directed against a polypeptide of the present invention, said polypeptide having the potential to elicit an allergic and/or immune response in an organism, and transforming the organism with said antibody gene such that it is expressed (e.g., constitutively, inducibly, etc.) in the organism. Thus, the organism would effectively become resistant to an allergic response resulting from the ingestion or presence of such an immune/allergic reactive polypeptide. Moreover, such a use of the antibodies of the present invention may have particular utility in preventing and/or ameliorating 20 autoimmune diseases and/or disorders, as such conditions are typically a result of antibodies being directed against endogenous proteins. For example, in the instance where the polypeptide of the present invention is responsible for modulating the immune response to auto-antigens, transforming the organism and/or individual with a construct comprising any of the promoters disclosed herein or otherwise known in 25 the art, in addition, to a polynucleotide encoding the antibody directed against the polypeptide of the present invention could effectively inhibit the organism's immune system from eliciting an immune response to the auto-antigen(s). Detailed 30 descriptions of therapeutic and/or gene therapy applications of the present invention are provided elsewhere herein.

35 Alternatively, antibodies of the present invention could be produced in a plant (e.g., cloning the gene of the antibody directed against a polypeptide of the present

5 invention, and transforming a plant with a suitable vector comprising said gene for constitutive expression of the antibody within the plant), and the plant subsequently ingested by an animal, thereby conferring temporary immunity to the animal for the specific antigen the antibody is directed towards (See, for example, US Patent Nos. 5,914,123 and 6,034,298).

10 In another embodiment, antibodies of the present invention, preferably polyclonal antibodies, more preferably monoclonal antibodies, and most preferably single-chain antibodies, can be used as a means of inhibiting gene expression of a particular gene, or genes, in a human, mammal, and/or other organism. See, for example, International Publication Number WO 00/05391, published 2/3/00, to Dow 15 Agrosciences LLC. The application of such methods for the antibodies of the present invention are known in the art, and are more particularly described elsewhere herein.

20 In yet another embodiment, antibodies of the present invention may be useful for multimerizing the polypeptides of the present invention. For example, certain proteins may confer enhanced biological activity when present in a multimeric state (i.e., such enhanced activity may be due to the increased effective concentration of such proteins whereby more protein is available in a localized location).

#### *Antibody-based Gene Therapy*

25 In a specific embodiment, nucleic acids comprising sequences encoding antibodies or functional derivatives thereof, are administered to treat, inhibit or prevent a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention, by way of gene therapy. Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic acid. In this embodiment of the invention, the nucleic acids produce their encoded 30 protein that mediates a therapeutic effect.

Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., Clinical Pharmacy 12:488-505 (1993); Wu and Wu, Biotherapy 3:87-95 (1991); 35 Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62:191-217

5 (1993); May, TIBTECH 11(5):155-215 (1993). Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); and Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990).

10 In a preferred aspect, the compound comprises nucleic acid sequences encoding an antibody, said nucleic acid sequences being part of expression vectors that express the antibody or fragments or chimeric proteins or heavy or light chains thereof in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the antibody coding region, said promoter being inducible or 15 constitutive, and, optionally, tissue- specific. In another particular embodiment, nucleic acid molecules are used in which the antibody coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the antibody encoding nucleic acids (Koller and Smithies, Proc. Natl. Acad. Sci. USA 20 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989). In specific embodiments, the expressed antibody molecule is a single chain antibody; alternatively, the nucleic acid sequences include sequences encoding both the heavy and light chains, or fragments thereof, of the antibody.

25 Delivery of the nucleic acids into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid- carrying vectors, or indirect, in which case, cells are first transformed with the nucleic acids in vitro, then transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

30 In a specific embodiment, the nucleic acid sequences are directly administered in vivo, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing them as part of an appropriate nucleic acid expression vector and administering it so that they become intracellular, e.g., by infection using defective or attenuated retrovirals or other viral vectors (see U.S. Patent No. 4,980,286), or by direct injection 35 of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents,

5 encapsulation in liposomes, microparticles, or microcapsules, or by administering them in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)) (which can be used to target cell types specifically expressing the receptors), etc. In another embodiment, nucleic acid-ligand  
10 complexes can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180; WO 92/22635; WO92/20316; WO93/14188, WO 93/20221). Alternatively,  
15 the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989)).

In a specific embodiment, viral vectors that contains nucleic acid sequences encoding an antibody of the invention are used. For example, a retroviral vector can  
20 be used (see Miller et al., Meth. Enzymol. 217:581-599 (1993)). These retroviral vectors contain the components necessary for the correct packaging of the viral genome and integration into the host cell DNA. The nucleic acid sequences encoding the antibody to be used in gene therapy are cloned into one or more vectors, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can  
25 be found in Boesen et al., Biotherapy 6:291-302 (1994), which describes the use of a retroviral vector to deliver the *mdrl* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., J. Clin. Invest. 93:644-651 (1994); Kiem et al., Blood 83:1467-1473 (1994); Salmons and Gunzberg, Human  
30 Gene Therapy 4:129-141 (1993); and Grossman and Wilson, Curr. Opin. in Genetics and Devel. 3:110-114 (1993).

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of  
35

5 being capable of infecting non-dividing cells. Kozarsky and Wilson, Current Opinion in Genetics and Development 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout et al., Human Gene Therapy 5:3-10 (1994) demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld 10 et al., Science 252:431-434 (1991); Rosenfeld et al., Cell 68:143- 155 (1992); Mastrangeli et al., J. Clin. Invest. 91:225-234 (1993); PCT Publication WO94/12649; and Wang, et al., Gene Therapy 2:775-783 (1995). In a preferred embodiment, adenovirus vectors are used.

15 Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., Proc. Soc. Exp. Biol. Med. 204:289-300 (1993); U.S. Patent No. 5,436,146).

20 Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to 25 isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a patient.

30 In this embodiment, the nucleic acid is introduced into a cell prior to administration *in vivo* of the resulting recombinant cell. Such introduction can be carried out by any method known in the art, including but not limited to transfection, 35 electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, Meth. Enzymol. 217:599-618 (1993); Cohen et al., Meth. Enzymol. 217:618-644 (1993); Cline, Pharmac. Ther. 29:69-92m (1985) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably heritable and expressible by its cell progeny.

5 The resulting recombinant cells can be delivered to a patient by various methods known in the art. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

10 Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes; blood cells such as Tlymphocytes, Blymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes; various stem or progenitor 15 cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, 20 nucleic acid sequences encoding an antibody are introduced into the cells such that they are expressible by the cells or their progeny, and the recombinant cells are then administered *in vivo* for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained *in vitro* can potentially be used in accordance with this embodiment of the 25 present invention (see e.g. PCT Publication WO 94/08598; Stemple and Anderson, Cell 71:973-985 (1992); Rheinwald, Meth. Cell Bio. 21A:229 (1980); and Pittelkow and Scott, Mayo Clinic Proc. 61:771 (1986)).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, 30 such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription. Demonstration of Therapeutic or Prophylactic Activity

The compounds or pharmaceutical compositions of the invention are preferably tested *in vitro*, and then *in vivo* for the desired therapeutic or prophylactic 35 activity, prior to use in humans. For example, *in vitro* assays to demonstrate the therapeutic or prophylactic utility of a compound or pharmaceutical composition

5 include, the effect of a compound on a cell line or a patient tissue sample. The effect of the compound or composition on the cell line and/or tissue sample can be determined utilizing techniques known to those of skill in the art including, but not limited to, rosette formation assays and cell lysis assays. In accordance with the invention, in vitro assays which can be used to determine whether administration of a  
10 specific compound is indicated, include in vitro cell culture assays in which a patient tissue sample is grown in culture, and exposed to or otherwise administered a compound, and the effect of such compound upon the tissue sample is observed.

*Therapeutic/Prophylactic Administration and Compositions*

15 The invention provides methods of treatment, inhibition and prophylaxis by administration to a subject of an effective amount of a compound or pharmaceutical composition of the invention, preferably an antibody of the invention. In a preferred aspect, the compound is substantially purified (e.g., substantially free from substances that limit its effect or produce undesired side-effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human.  
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Formulations and methods of administration that can be employed when the compound comprises a nucleic acid or an immunoglobulin are described above; additional appropriate formulations and routes of administration can be selected from among those described herein below.

Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)),  
30 construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds or compositions may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g.,  
35 oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition,

5 it may be desirable to introduce the pharmaceutical compounds or compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an  
10 inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compounds or compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after  
15 surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. Preferably, when administering a protein, including an antibody, of the invention, care must be taken to use materials to which the protein does not absorb.

20 In another embodiment, the compound or composition can be delivered in a vesicle, in particular a liposome (see Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353- 365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

25 In yet another embodiment, the compound or composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.* 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)). In another embodiment, polymeric materials can be used (see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, *J. Macromol. Sci. Rev. Macromol. Chem.* 23:61 (1983); see also Levy et al., *Science* 228:190 (1985); During et al., *Ann. Neurol.* 25:351 (1989); Howard et al., *J. Neurosurg.* 71:105 (1989)). In yet  
30 another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose  
35

5 (see, e.g., Goodson, in *Medical Applications of Controlled Release*, supra, vol. 2, pp. 115-138 (1984)).

Other controlled release systems are discussed in the review by Langer (Science 249:1527-1533 (1990)).

In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered *in vivo* to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating 15 with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (see e.g., Joliot et al., Proc. Natl. Acad. Sci. USA 88:1864-1868 (1991)), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

20 The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a compound, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized 25 pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred 30 carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, 35 glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering

5 agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium 10 saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the 15 mode of administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the 20 composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the 25 composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The compounds of the invention can be formulated as neutral or salt forms. 30 Pharmaceutically acceptable salts include those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

35 The amount of the compound of the invention which will be effective in the treatment, inhibition and prevention of a disease or disorder associated with aberrant

5 expression and/or activity of a polypeptide of the invention can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the  
10 practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

For antibodies, the dosage administered to a patient is typically 0.1 mg/kg to 100 mg/kg of the patient's body weight. Preferably, the dosage administered to a patient is between 0.1 mg/kg and 20 mg/kg of the patient's body weight, more  
15 preferably 1 mg/kg to 10 mg/kg of the patient's body weight. Generally, human antibodies have a longer half-life within the human body than antibodies from other species due to the immune response to the foreign polypeptides. Thus, lower dosages of human antibodies and less frequent administration is often possible. Further, the dosage and frequency of administration of antibodies of the invention may be reduced  
20 by enhancing uptake and tissue penetration (e.g., into the brain) of the antibodies by modifications such as, for example, lipidation.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a  
25 notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

#### *Diagnosis and Imaging With Antibodies*

30 Labeled antibodies, and derivatives and analogs thereof, which specifically bind to a polypeptide of interest can be used for diagnostic purposes to detect, diagnose, or monitor diseases, disorders, and/or conditions associated with the aberrant expression and/or activity of a polypeptide of the invention. The invention provides for the detection of aberrant expression of a polypeptide of interest,  
35 comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest

5 and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of aberrant expression.

10 The invention provides a diagnostic assay for diagnosing a disorder, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a particular disorder. With 15 respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

20 Antibodies of the invention can be used to assay protein levels in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., *J. Cell. Biol.* 101:976-985 (1985); Jalkanen, et al., *J. Cell. Biol.* 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked 25 immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99Tc); luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

30 One aspect of the invention is the detection and diagnosis of a disease or disorder associated with aberrant expression of a polypeptide of interest in an animal, preferably a mammal and most preferably a human. In one embodiment, diagnosis comprises: a) administering (for example, parenterally, subcutaneously, or intraperitoneally) to a subject an effective amount of a labeled molecule which 35 specifically binds to the polypeptide of interest; b) waiting for a time interval following the administering for permitting the labeled molecule to preferentially

5 concentrate at sites in the subject where the polypeptide is expressed (and for unbound labeled molecule to be cleared to background level); c) determining background level; and d) detecting the labeled molecule in the subject, such that detection of labeled molecule above the background level indicates that the subject has a particular disease or disorder associated with aberrant expression of the  
10 polypeptide of interest. Background level can be determined by various methods including, comparing the amount of labeled molecule detected to a standard value previously determined for a particular system.

It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce  
15 diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of  
20 Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).

Depending on several variables, including the type of label used and the mode of administration, the time interval following the administration for permitting the  
25 labeled molecule to preferentially concentrate at sites in the subject and for unbound labeled molecule to be cleared to background level is 6 to 48 hours or 6 to 24 hours or 6 to 12 hours. In another embodiment the time interval following administration is 5 to 20 days or 5 to 10 days.

In an embodiment, monitoring of the disease or disorder is carried out by  
30 repeating the method for diagnosing the disease or disease, for example, one month after initial diagnosis, six months after initial diagnosis, one year after initial diagnosis, etc.

Presence of the labeled molecule can be detected in the patient using methods known in the art for in vivo scanning. These methods depend upon the type of label  
35 used. Skilled artisans will be able to determine the appropriate method for detecting a particular label. Methods and devices that may be used in the diagnostic methods of

5 the invention include, but are not limited to, computed tomography (CT), whole body scan such as position emission tomography (PET), magnetic resonance imaging (MRI), and sonography.

In a specific embodiment, the molecule is labeled with a radioisotope and is detected in the patient using a radiation responsive surgical instrument (Thurston et 10 al., U.S. Patent No. 5,441,050). In another embodiment, the molecule is labeled with a fluorescent compound and is detected in the patient using a fluorescence responsive scanning instrument. In another embodiment, the molecule is labeled with a positron emitting metal and is detected in the patient using positron emission-tomography. In yet another embodiment, the molecule is labeled with a paramagnetic label and is 15 detected in a patient using magnetic resonance imaging (MRI).

#### *Kits*

The present invention provides kits that can be used in the above methods. In one embodiment, a kit comprises an antibody of the invention, preferably a purified antibody, in one or more containers. In a specific embodiment, the kits of the present 20 invention contain a substantially isolated polypeptide comprising an epitope which is specifically immunoreactive with an antibody included in the kit. Preferably, the kits of the present invention further comprise a control antibody which does not react with the polypeptide of interest. In another specific embodiment, the kits of the present invention contain a means for detecting the binding of an antibody to a polypeptide of 25 interest (e.g., the antibody may be conjugated to a detectable substrate such as a fluorescent compound, an enzymatic substrate, a radioactive compound or a luminescent compound, or a second antibody which recognizes the first antibody may be conjugated to a detectable substrate).

In another specific embodiment of the present invention, the kit is a diagnostic 30 kit for use in screening serum containing antibodies specific against proliferative and/or cancerous polynucleotides and polypeptides. Such a kit may include a control antibody that does not react with the polypeptide of interest. Such a kit may include a substantially isolated polypeptide antigen comprising an epitope which is specifically immunoreactive with at least one anti-polypeptide antigen antibody. Further, such a 35 kit includes means for detecting the binding of said antibody to the antigen (e.g., the antibody may be conjugated to a fluorescent compound such as fluorescein or

5 rhodamine which can be detected by flow cytometry). In specific embodiments, the kit may include a recombinantly produced or chemically synthesized polypeptide antigen. The polypeptide antigen of the kit may also be attached to a solid support.

In a more specific embodiment the detecting means of the above-described kit includes a solid support to which said polypeptide antigen is attached. Such a kit may 10 also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the polypeptide antigen can be detected by binding of the said reporter-labeled antibody.

In an additional embodiment, the invention includes a diagnostic kit for use in screening serum containing antigens of the polypeptide of the invention. The 15 diagnostic kit includes a substantially isolated antibody specifically immunoreactive with polypeptide or polynucleotide antigens, and means for detecting the binding of the polynucleotide or polypeptide antigen to the antibody. In one embodiment, the antibody is attached to a solid support. In a specific embodiment, the antibody may be a monoclonal antibody. The detecting means of the kit may include a second, labeled 20 monoclonal antibody. Alternatively, or in addition, the detecting means may include a labeled, competing antigen.

In one diagnostic configuration, test serum is reacted with a solid phase reagent having a surface-bound antigen obtained by the methods of the present invention. After binding with specific antigen antibody to the reagent and removing 25 unbound serum components by washing, the reagent is reacted with reporter-labeled anti-human antibody to bind reporter to the reagent in proportion to the amount of bound anti-antigen antibody on the solid support. The reagent is again washed to remove unbound labeled antibody, and the amount of reporter associated with the reagent is determined. Typically, the reporter is an enzyme which is detected by 30 incubating the solid phase in the presence of a suitable fluorometric, luminescent or colorimetric substrate (Sigma, St. Louis, MO).

The solid surface reagent in the above assay is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plate or filter material. These attachment methods generally include 35 non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the

5 solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

10 Thus, the invention provides an assay system or kit for carrying out this diagnostic method. The kit generally includes a support with surface- bound recombinant antigens, and a reporter-labeled anti-human antibody for detecting surface-bound anti-antigen antibody.

### Fusion Proteins

15 Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because certain proteins target cellular locations based on trafficking signals, the polypeptides of the present 20 invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

25 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Peptide moieties may be added to the polypeptide 30 to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. Similarly, peptide cleavage sites can be introduced in-between such peptide moieties, which could additionally be subjected to protease activity to remove said peptide(s) from the protein of the present invention. The addition of peptide moieties, including peptide cleavage sites, to facilitate handling of polypeptides are 35 familiar and routine techniques in the art.

5 Moreover, polypeptides of the present invention, including fragments, and  
specifically epitopes, can be combined with parts of the constant domain of  
immunoglobulins (IgA, IgE, IgG, IgM) or portions thereof (CH1, CH2, CH3, and any  
combination thereof, including both entire domains and portions thereof), resulting in  
chimeric polypeptides. These fusion proteins facilitate purification and show an  
10 increased half-life in vivo. One reported example describes chimeric proteins  
consisting of the first two domains of the human CD4-polypeptide and various  
domains of the constant regions of the heavy or light chains of mammalian  
immunoglobulins. (EP A 394,827; Traunecker et al., *Nature* 331:84-86 (1988).)  
Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be  
15 more efficient in binding and neutralizing other molecules, than the monomeric  
secreted protein or protein fragment alone. (Fountoulakis et al., *J. Biochem.*  
270:3958-3964 (1995).)

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion  
proteins comprising various portions of the constant region of immunoglobulin  
20 molecules together with another human protein or part thereof. In many cases, the Fc  
part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in,  
for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively,  
deleting the Fc part after the fusion protein has been expressed, detected, and purified,  
would be desired. For example, the Fc portion may hinder therapy and diagnosis if the  
25 fusion protein is used as an antigen for immunizations. In drug discovery, for  
example, human proteins, such as hIL-5, have been fused with Fc portions for the  
purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D.  
Bennett et al., *J. Molecular Recognition* 8:52-58 (1995); K. Johanson et al., *J. Biol.  
Chem.* 270:9459-9471 (1995).)

30 Moreover, the polypeptides of the present invention can be fused to marker  
sequences (also referred to as "tags"). Due to the availability of antibodies specific to  
such "tags", purification of the fused polypeptide of the invention, and/or its  
identification is significantly facilitated since antibodies specific to the polypeptides  
of the invention are not required. Such purification may be in the form of an affinity  
35 purification whereby an anti-tag antibody or another type of affinity matrix (e.g., anti-  
tag antibody attached to the matrix of a flow-thru column) that binds to the epitope

5 tag is present. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion 10 protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984)).

The skilled artisan would acknowledge the existence of other "tags" which could be readily substituted for the tags referred to supra for purification and/or 15 identification of polypeptides of the present invention (Jones C., et al., J Chromatogr A. 707(1):3-22 (1995)). For example, the c-myc tag and the 8F9, 3C7, 6E10, G4m B7 and 9E10 antibodies thereto (Evan et al., Molecular and Cellular Biology 5:3610-3616 (1985)); the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky et al., Protein Engineering, 3(6):547-553 (1990), the Flag-peptide - i.e., the 20 octapeptide sequence DYKDDDDK (SEQ ID NO:36), (Hopp et al., Biotech. 6:1204-1210 (1988); the KT3 epitope peptide (Martin et al., Science, 255:192-194 (1992)); a-tubulin epitope peptide (Skinner et al., J. Biol. Chem., 266:15136-15166, (1991)); the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al., Proc. Natl. Sci. USA, 87:6363-6397 (1990)), the FITC epitope (Zymed, Inc.), the GFP epitope (Zymed, 25 Inc.), and the Rhodamine epitope (Zymed, Inc.).

The present invention also encompasses the attachment of up to nine codons encoding a repeating series of up to nine arginine amino acids to the coding region of a polynucleotide of the present invention. The invention also encompasses chemically derivitizing a polypeptide of the present invention with a repeating series of up to nine 30 arginine amino acids. Such a tag, when attached to a polypeptide, has recently been shown to serve as a universal pass, allowing compounds access to the interior of cells without additional derivitization or manipulation (Wender, P., et al., unpublished data).

Protein fusions involving polypeptides of the present invention, including 35 fragments and/or variants thereof, can be used for the following, non-limiting examples, subcellular localization of proteins, determination of protein-protein

5 interactions via immunoprecipitation, purification of proteins via affinity chromatography, functional and/or structural characterization of protein. The present invention also encompasses the application of hapten specific antibodies for any of the uses referenced above for epitope fusion proteins. For example, the polypeptides of the present invention could be chemically derivatized to attach hapten molecules  
10 (e.g., DNP, (Zymed, Inc.)). Due to the availability of monoclonal antibodies specific to such haptens, the protein could be readily purified using immunoprecipitation, for example.

15 Polypeptides of the present invention, including fragments and/or variants thereof, in addition to, antibodies directed against such polypeptides, fragments, and/or variants, may be fused to any of a number of known, and yet to be determined, toxins, such as ricin, saporin (Mashiba H, et al., Ann. N. Y. Acad. Sci. 1999;886:233-5), or HC toxin (Tonukari NJ, et al., Plant Cell. 2000 Feb;12(2):237-248), for example. Such fusions could be used to deliver the toxins to desired tissues for which a ligand or a protein capable of binding to the polypeptides of the invention exists.

20 The invention encompasses the fusion of antibodies directed against polypeptides of the present invention, including variants and fragments thereof, to said toxins for delivering the toxin to specific locations in a cell, to specific tissues, and/or to specific species. Such bifunctional antibodies are known in the art, though a review describing additional advantageous fusions, including citations for methods of  
25 production, can be found in P.J. Hudson, Curr. Opp. In. Imm. 11:548-557, (1999); this publication, in addition to the references cited therein, are hereby incorporated by reference in their entirety herein. In this context, the term "toxin" may be expanded to include any heterologous protein, a small molecule, radionucleotides, cytotoxic drugs, liposomes, adhesion molecules, glycoproteins, ligands, cell or tissue-specific ligands,  
30 enzymes, of bioactive agents, biological response modifiers, anti-fungal agents, hormones, steroids, vitamins, peptides, peptide analogs, anti-allergenic agents, anti-tubercular agents, anti-viral agents, antibiotics, anti-protozoan agents, chelates, radioactive particles, radioactive ions, X-ray contrast agents, monoclonal antibodies, polyclonal antibodies and genetic material. In view of the present disclosure, one  
35 skilled in the art could determine whether any particular "toxin" could be used in the compounds of the present invention. Examples of suitable "toxins" listed above are

5 exemplary only and are not intended to limit the "toxins" that may be used in the present invention.

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

## 10 **Vectors, Host Cells, and Protein Production**

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In 15 the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the 20 vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli* lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to 25 name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or 30 UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of 35 appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells

5 (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris* (ATCC Accession No. 201178)); insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture media and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-10 9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16A, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available 15 from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlsbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

20 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., *Basic Methods In Molecular Biology* (1986). It is specifically contemplated that the 25 polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, 30 phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

35 Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical

5 synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also 10 include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some 15 proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express the polypeptide of the present invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A 20 main step in the methanol metabolism pathway is the oxidation of methanol to formaldehyde using O<sub>2</sub>. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for O<sub>2</sub>. Consequently, in a growth medium depending on methanol as a main 25 carbon source, the promoter region of one of the two alcohol oxidase genes (AOX1) is highly active. In the presence of methanol, alcohol oxidase produced from the AOX1 gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. See, Ellis, S.B., et al., Mol. Cell. Biol. 5:1111-21 (1985); Koutz, P.J., et al., Yeast 5:167-77 (1989); Tschopp, J.F., et al., Nucl. Acids Res. 15:3859-76 (1987). 30 Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the AOX1 regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

In one example, the plasmid vector pPIC9K is used to express DNA encoding 35 a polypeptide of the invention, as set forth herein, in a *Pichia* yeast system essentially as described in "Pichia Protocols: Methods in Molecular Biology," D.R. Higgins and

5 J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a protein of the invention by virtue of the strong AOX1 promoter linked to the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

10 Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG, as required.

15 In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

20 In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide 25 sequences) that is operably associated with the polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination, resulting in the formation of a new transcription unit 30 (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; U.S. Patent No. 5,733,761, issued March 31, 1998; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 35 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

In addition, polypeptides of the invention can be chemically synthesized using

5 techniques known in the art (e.g., see Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman & Co., N.Y., and Hunkapiller et al., *Nature*, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide sequence of the invention can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid  
10 analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, a-amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine,  
15 norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoroo-  
amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the  
amino acid can be D (dextrorotary) or L (levorotary).

20 The invention encompasses polypeptides which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not  
25 limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH4; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-  
30 terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and  
35 isolation of the protein, the addition of epitope tagged peptide fragments (e.g., FLAG, HA, GST, thioredoxin, maltose binding protein, etc.), attachment of affinity tags such

5 as biotin and/or streptavidin, the covalent attachment of chemical moieties to the amino acid backbone, N- or C-terminal processing of the polypeptides ends (e.g., proteolytic processing), deletion of the N-terminal methionine residue, etc.

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as  
10 increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent NO: 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random  
15 positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The invention further encompasses chemical derivitization of the polypeptides of the present invention, preferably where the chemical is a hydrophilic polymer residue. Exemplary hydrophilic polymers, including derivatives, may be those that  
20 include polymers in which the repeating units contain one or more hydroxy groups (polyhydroxy polymers), including, for example, poly(vinyl alcohol); polymers in which the repeating units contain one or more amino groups (polyamine polymers), including, for example, peptides, polypeptides, proteins and lipoproteins, such as albumin and natural lipoproteins; polymers in which the repeating units contain one or  
25 more carboxy groups (polycarboxy polymers), including, for example, carboxymethylcellulose, alginic acid and salts thereof, such as sodium and calcium alginate, glycosaminoglycans and salts thereof, including salts of hyaluronic acid, phosphorylated and sulfonated derivatives of carbohydrates, genetic material, such as interleukin-2 and interferon, and phosphorothioate oligomers; and polymers in which  
30 the repeating units contain one or more saccharide moieties (polysaccharide polymers), including, for example, carbohydrates.

The molecular weight of the hydrophilic polymers may vary, and is generally about 50 to about 5,000,000, with polymers having a molecular weight of about 100 to about 50,000 being preferred. The polymers may be branched or unbranched. More  
35 preferred polymers have a molecular weight of about 150 to about 10,000, with molecular weights of 200 to about 8,000 being even more preferred.

5 For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release  
10 desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog).

Additional preferred polymers which may be used to derivatize polypeptides of the invention, include, for example, poly(ethylene glycol) (PEG),  
15 poly(vinylpyrrolidine), polyoxomers, polysorbate and poly(vinyl alcohol), with PEG polymers being particularly preferred. Preferred among the PEG polymers are PEG polymers having a molecular weight of from about 100 to about 10,000. More preferably, the PEG polymers have a molecular weight of from about 200 to about 8,000, with PEG 2,000, PEG 5,000 and PEG 8,000, which have molecular weights of  
20 2,000, 5,000 and 8,000, respectively, being even more preferred. Other suitable hydrophilic polymers, in addition to those exemplified above, will be readily apparent to one skilled in the art based on the present disclosure. Generally, the polymers used may include polymers that can be attached to the polypeptides of the invention via alkylation or acylation reactions.

25 The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik et al., *Exp. Hematol.* 20:1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues;  
30 those having a free carboxyl group may include aspartic acid residues glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used  
35

5 as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may 10 select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this 15 moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminus) available for 20 derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

As with the various polymers exemplified above, it is contemplated that the polymeric residues may contain functional groups in addition, for example, to those 25 typically involved in linking the polymeric residues to the polypeptides of the present invention. Such functionalities include, for example, carboxyl, amine, hydroxy and thiol groups. These functional groups on the polymeric residues can be further reacted, if desired, with materials that are generally reactive with such functional groups and which can assist in targeting specific tissues in the body including, for 30 example, diseased tissue. Exemplary materials which can be reacted with the additional functional groups include, for example, proteins, including antibodies, carbohydrates, peptides, glycopeptides, glycolipids, lectins, and nucleosides.

In addition to residues of hydrophilic polymers, the chemical used to derivatize the polypeptides of the present invention can be a saccharide residue. 35 Exemplary saccharides which can be derived include, for example, monosaccharides or sugar alcohols, such as erythrose, threose, ribose, arabinose, xylose, lyxose,

5 fructose, sorbitol, mannitol and sedoheptulose, with preferred monosaccharides being fructose, mannose, xylose, arabinose, mannitol and sorbitol; and disaccharides, such as lactose, sucrose, maltose and cellobiose. Other saccharides include, for example, inositol and ganglioside head groups. Other suitable saccharides, in addition to those exemplified above, will be readily apparent to one skilled in the art based on the  
10 present disclosure. Generally, saccharides which may be used for derivitization include saccharides that can be attached to the polypeptides of the invention via alkylation or acylation reactions.

Moreover, the invention also encompasses derivitization of the polypeptides of the present invention, for example, with lipids (including cationic, anionic, 15 polymerized, charged, synthetic, saturated, unsaturated, and any combination of the above, etc.). stabilizing agents.

The invention encompasses derivitization of the polypeptides of the present invention, for example, with compounds that may serve a stabilizing function (e.g., to increase the polypeptides half-life in solution, to make the polypeptides more water 20 soluble, to increase the polypeptides hydrophilic or hydrophobic character, etc.). Polymers useful as stabilizing materials may be of natural, semi-synthetic (modified natural) or synthetic origin. Exemplary natural polymers include naturally occurring polysaccharides, such as, for example, arabinans, fructans, fucans, galactans, galacturonans, glucans, mannans, xylans (such as, for example, inulin), levan, 25 fucoidan, carrageenan, galatocarolose, pectic acid, pectins, including amylose, pullulan, glycogen, amylopectin, cellulose, dextran, dextrin, dextrose, glucose, polyglucose, polydextrose, pustulan, chitin, agarose, keratin, chondroitin, dermatan, hyaluronic acid, alginic acid, xanthin gum, starch and various other natural homopolymer or heteropolymers, such as those containing one or more of the 30 following aldoses, ketoses, acids or amines: erythrose, threose, ribose, arabinose, xylose, lyxose, allose, altrose, glucose, dextrose, mannose, gulose, idose, galactose, talose, erythrulose, ribulose, xylulose, psicose, fructose, sorbose, tagatose, mannitol, sorbitol, lactose, sucrose, trehalose, maltose, cellobiose, glycine, serine, threonine, cysteine, tyrosine, asparagine, glutamine, aspartic acid, glutamic acid, lysine, 35 arginine, histidine, glucuronic acid, gluconic acid, glucaric acid, galacturonic acid, mannuronic acid, glucosamine, galactosamine, and neuraminic acid, and naturally

5 occurring derivatives thereof. Accordingly, suitable polymers include, for example, proteins, such as albumin, polyalginates, and polylactide-coglycolide polymers. Exemplary semi-synthetic polymers include carboxymethylcellulose, hydroxymethylcellulose, hydroxypropylmethylcellulose, methylcellulose, and methoxycellulose. Exemplary synthetic polymers include polyphosphazenes, 10 hydroxyapatites, fluoroapatite polymers, polyethylenes (such as, for example, polyethylene glycol (including for example, the class of compounds referred to as Pluronics.RTM., commercially available from BASF, Parsippany, N.J.), polyoxyethylene, and polyethylene terephthalate), polypropylenes (such as, for example, polypropylene glycol), polyurethanes (such as, for example, polyvinyl 15 alcohol (PVA), polyvinyl chloride and polyvinylpyrrolidone), polyamides including nylon, polystyrene, polylactic acids, fluorinated hydrocarbon polymers, fluorinated carbon polymers (such as, for example, polytetrafluoroethylene), acrylate, methacrylate, and polymethylmethacrylate, and derivatives thereof. Methods for the preparation of derivatized polypeptides of the invention which employ polymers as 20 stabilizing compounds will be readily apparent to one skilled in the art, in view of the present disclosure, when coupled with information known in the art, such as that described and referred to in Unger, U.S. Pat. No. 5,205,290, the disclosure of which is hereby incorporated by reference herein in its entirety.

Moreover, the invention encompasses additional modifications of the 25 polypeptides of the present invention. Such additional modifications are known in the art, and are specifically provided, in addition to methods of derivitization, etc., in US Patent No. 6,028,066, which is hereby incorporated in its entirety herein.

The polypeptides of the invention may be in monomers or multimers (i.e., dimers, trimers, tetramers and higher multimers). Accordingly, the present invention 30 relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, Therapeutics) containing them. In specific embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

35 Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer, refers to a multimer containing only polypeptides

5 corresponding to the amino acid sequence of SEQ ID NO:Y or encoded by the cDNA contained in a deposited clone (including fragments, variants, splice variants, and fusion proteins, corresponding to these polypeptides as described herein). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer  
10 containing only polypeptides having an identical amino acid sequence. In another specific embodiment, a homomer of the invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (e.g., containing polypeptides having identical or different amino acid sequences) or a homotrimer (e.g., containing polypeptides having identical and/or different amino acid sequences). In additional  
15 embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (i.e., polypeptides of different proteins) in addition to  
20 the polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer.

Multimers of the invention may be the result of hydrophobic, hydrophilic,  
25 ionic and/or covalent associations and/or may be indirectly linked, by for example, liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for example, heterotrimers or heterotetramers, are formed  
30 when polypeptides of the invention contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the invention are formed by covalent associations with and/or between the polypeptides of the invention. Such covalent associations may involve one or more amino acid residues contained in the polypeptide sequence (e.g., that recited in the sequence listing, or contained in the polypeptide encoded by a deposited clone). In one instance,  
35

5 the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide  
10 sequence in a fusion protein of the invention.

In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In a specific example, the covalent associations are between the heterologous sequence contained in an Fc fusion protein of the invention (as described  
15 herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another protein that is capable of forming covalently associated multimers, such as for example, osteoprotegerin (see, e.g., International Publication NO: WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another embodiment,  
20 two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

25 Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper polypeptide sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science  
30 240:1759, (1988)), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion  
35 proteins comprising a polypeptide of the invention fused to a polypeptide sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the

5 resulting soluble multimeric fusion protein is recovered from the culture supernatant using techniques known in the art.

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung 10 surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S. patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

In another example, proteins of the invention are associated by interactions 15 between Flag® polypeptide sequence contained in fusion proteins of the invention containing Flag® polypeptide sequence. In a further embodiment, associations proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in Flag® fusion proteins of the invention and anti-Flag® antibody.

20 The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

25 Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely

30 modified by the addition of cysteine or biotin to the C terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the 35 polypeptide components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its

5 entirety).

Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent 10 Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic polynucleotide encoding the translated product of the polypeptide in the reverse 15 orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hydrophobic or signal 20 peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

In addition, the polynucleotide insert of the present invention could be operatively linked to "artificial" or chimeric promoters and transcription factors. 25 Specifically, the artificial promoter could comprise, or alternatively consist, of any combination of cis-acting DNA sequence elements that are recognized by trans-acting transcription factors. Preferably, the cis acting DNA sequence elements and trans-acting transcription factors are operable in mammals. Further, the trans-acting transcription factors of such "artificial" promoters could also be "artificial" or 30 chimeric in design themselves and could act as activators or repressors to said "artificial" promoter.

## 5 Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include *in situ* hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence *in situ* hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides

5 correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage 10 analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. Disease mapping data are known in the art. Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

15 Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected organisms can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed 20 in some or all affected organisms, but not in normal organisms, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal organisms is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

25 Furthermore, increased or decreased expression of the gene in affected organisms as compared to unaffected organisms can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

30 Thus, the invention also provides a diagnostic method useful during diagnosis of a disorder, involving measuring the expression level of polynucleotides of the present invention in cells or body fluid from an organism and comparing the measured gene expression level with a standard level of polynucleotide expression level, whereby an increase or decrease in the gene expression level compared to the 35 standard is indicative of a disorder.

5 By "measuring the expression level of a polynucleotide of the present invention" is intended qualitatively or quantitatively measuring or estimating the level of the polypeptide of the present invention or the level of the mRNA encoding the polypeptide in a first biological sample either directly (e.g., by determining or estimating absolute protein level or mRNA level) or relatively (e.g., by comparing to  
10 the polypeptide level or mRNA level in a second biological sample). Preferably, the polypeptide level or mRNA level in the first biological sample is measured or estimated and compared to a standard polypeptide level or mRNA level, the standard being taken from a second biological sample obtained from an individual not having the disorder or being determined by averaging levels from a population of organisms  
15 not having a disorder. As will be appreciated in the art, once a standard polypeptide level or mRNA level is known, it can be used repeatedly as a standard for comparison.

By "biological sample" is intended any biological sample obtained from an organism, body fluids, cell line, tissue culture, or other source which contains the  
20 polypeptide of the present invention or mRNA. As indicated, biological samples include body fluids (such as the following non-limiting examples, sputum, amniotic fluid, urine, saliva, breast milk, secretions, interstitial fluid, blood, serum, spinal fluid, etc.) which contain the polypeptide of the present invention, and other tissue sources found to express the polypeptide of the present invention. Methods for obtaining  
25 tissue biopsies and body fluids from organisms are well known in the art. Where the biological sample is to include mRNA, a tissue biopsy is the preferred source.

The method(s) provided above may preferably be applied in a diagnostic method and/or kits in which polynucleotides and/or polypeptides are attached to a solid support. In one exemplary method, the support may be a "gene chip" or a  
30 "biological chip" as described in US Patents 5,837,832, 5,874,219, and 5,856,174. Further, such a gene chip with polynucleotides of the present invention attached may be used to identify polymorphisms between the polynucleotide sequences, with polynucleotides isolated from a test subject. The knowledge of such polymorphisms (i.e. their location, as well as, their existence) would be beneficial in identifying  
35 disease loci for many disorders, including proliferative diseases and conditions. Such

5 a method is described in US Patents 5,858,659 and 5,856,104. The US Patents referenced supra are hereby incorporated by reference in their entirety herein.

The present invention encompasses polynucleotides of the present invention that are chemically synthesized, or reproduced as peptide nucleic acids (PNA), or according to other methods known in the art. The use of PNAs would serve as the 10 preferred form if the polynucleotides are incorporated onto a solid support, or gene chip. For the purposes of the present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine, thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus oxides, or deoxyribose 15 derivatives, are not present in PNAs. As disclosed by P. E. Nielsen, M. Egholm, R. H. Berg and O. Buchardt, *Science* 254, 1497 (1991); and M. Egholm, O. Buchardt, L. Christensen, C. Behrens, S. M. Freier, D. A. Driver, R. H. Berg, S. K. Kim, B. Norden, and P. E. Nielsen, *Nature* 365, 666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact, 20 PNA binds more strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the 25 stronger binding characteristics of PNA:DNA hybrids. In addition, it is more likely that single base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point (T<sub>sub.m</sub>) by 8°- 20° C, vs. 4°-16° C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce 30 possible interference by salt during the analysis.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Antisense techniques are discussed, for example, in Okano, *J. Neurochem.* 56: 560 (1991); "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression", CRC Press, 35 Boca Raton, FL (1988). Triple helix formation is discussed in, for instance Lee et al., *Nucleic Acids Research* 6: 3073 (1979); Cooney et al., *Science* 241: 456 (1988); and

5 Dervan et al., *Science* 251: 1360 (1991). Both methods rely on binding of the polynucleotide to a complementary DNA or RNA. For these techniques, preferred polynucleotides are usually oligonucleotides 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., *Nucl. Acids Res.* 6:3073 (1979); Cooney et al., *Science* 241:456 (1988);  
10 and Dervan et al., *Science* 251:1360 (1991) ) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both  
15 techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat or prevent disease.

The present invention encompasses the addition of a nuclear localization signal, operably linked to the 5' end, 3' end, or any location therein, to any of the  
20 oligonucleotides, antisense oligonucleotides, triple helix oligonucleotides, ribozymes, PNA oligonucleotides, and/or polynucleotides, of the present invention. See, for example, G. Cutrona, et al., *Nat. Biotech.*, 18:300-303, (2000); which is hereby incorporated herein by reference.

Polynucleotides of the present invention are also useful in gene therapy. One  
25 goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell. In one example, polynucleotide  
30 sequences of the present invention may be used to construct chimeric RNA/DNA oligonucleotides corresponding to said sequences, specifically designed to induce host cell mismatch repair mechanisms in an organism upon systemic injection, for example (Bartlett, R.J., et al., *Nat. Biotech.*, 18:615-622 (2000), which is hereby incorporated by reference herein in its entirety). Such RNA/DNA oligonucleotides could be  
35 designed to correct genetic defects in certain host strains, and/or to introduce desired phenotypes in the host (e.g., introduction of a specific polymorphism within an

5 endogenous gene corresponding to a polynucleotide of the present invention that may ameliorate and/or prevent a disease symptom and/or disorder, etc.). Alternatively, the polynucleotide sequence of the present invention may be used to construct duplex oligonucleotides corresponding to said sequence, specifically designed to correct genetic defects in certain host strains, and/or to introduce desired phenotypes into the  
10 host (e.g., introduction of a specific polymorphism within an endogenous gene corresponding to a polynucleotide of the present invention that may ameliorate and/or prevent a disease symptom and/or disorder, etc). Such methods of using duplex oligonucleotides are known in the art and are encompassed by the present invention (see EP1007712, which is hereby incorporated by reference herein in its entirety).

15 The polynucleotides are also useful for identifying organisms from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for  
20 identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

25 The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an organisms genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, organisms can be identified because each organism will have a unique set  
30 of DNA sequences. Once an unique ID database is established for an organism, positive identification of that organism, living or dead, can be made from extremely small tissue samples. Similarly, polynucleotides of the present invention can be used as polymorphic markers, in addition to, the identification of transformed or non-transformed cells and/or tissues.

35 There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or

5 primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination. Moreover, as mentioned above, such reagents can be used to screen and/or identify transformed and non-transformed cells and/or tissues.

10 In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA 15 antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

### Uses of the Polypeptides

20 Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell. Biol. 105:3087-25 3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and 30 technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying protein levels in a biological sample, proteins can also be detected *in vivo* by imaging. Antibody labels or markers for *in vivo* imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, 35 suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and

5 ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example,  $^{131}\text{I}$ ,  $^{112}\text{In}$ ,  $^{99\text{m}}\text{Tc}$ ), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of  $^{99\text{m}}\text{Tc}$ . The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Moreover, polypeptides of the present invention can be used to treat, prevent, and/or diagnose disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different

5 polypeptide (e.g., hemoglobin S for hemoglobin B, SOD, catalase, DNA repair proteins), to inhibit the activity of a polypeptide (e.g., an oncogene or tumor suppressor), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a  
10 desired response (e.g., blood vessel growth inhibition, enhancement of the immune response to proliferative cells or tissues).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat, prevent, and/or diagnose disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce  
15 overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration  
20 columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

25

### Gene Therapy Methods

Another aspect of the present invention is to gene therapy methods for treating or preventing disorders, diseases and conditions. The gene therapy methods relate to the introduction of nucleic acid (DNA, RNA and antisense DNA or RNA) sequences  
30 into an animal to achieve expression of a polypeptide of the present invention. This method requires a polynucleotide which codes for a polypeptide of the invention that operatively linked to a promoter and any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques are known in the art, see, for example, WO90/11092, which is herein  
35 incorporated by reference.

Thus, for example, cells from a patient may be engineered with a

5 polynucleotide (DNA or RNA) comprising a promoter operably linked to a polynucleotide of the invention *ex vivo*, with the engineered cells then being provided to a patient to be treated with the polypeptide. Such methods are well-known in the art. For example, see Belldegrun et al., *J. Natl. Cancer Inst.*, 85:207-216 (1993); Ferrantini et al., *Cancer Research*, 53:107-1112 (1993); Ferrantini et al., *J. 10 Immunology* 153: 4604-4615 (1994); Kaido, T., et al., *Int. J. Cancer* 60: 221-229 (1995); Ogura et al., *Cancer Research* 50: 5102-5106 (1990); Santodonato, et al., *Human Gene Therapy* 7:1-10 (1996); Santodonato, et al., *Gene Therapy* 4:1246-1255 (1997); and Zhang, et al., *Cancer Gene Therapy* 3: 31-38 (1996)), which are herein incorporated by reference. In one embodiment, the cells which are engineered are 15 arterial cells. The arterial cells may be reintroduced into the patient through direct injection to the artery, the tissues surrounding the artery, or through catheter injection.

As discussed in more detail below, the polynucleotide constructs can be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, 20 and the like). The polynucleotide constructs may be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

In one embodiment, the polynucleotide of the invention is delivered as a naked polynucleotide. The term "naked" polynucleotide, DNA or RNA refers to sequences that are free from any delivery vehicle that acts to assist, promote or facilitate entry 25 into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the invention can also be delivered in liposome formulations and lipofectin formulations and the like can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in U.S. Patent Nos. 5,593,972, 5,589,466, and 30 5,580,859, which are herein incorporated by reference.

The polynucleotide vector constructs of the invention used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Appropriate vectors include pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; pSVK3, 35 pBPV, pMSG and pSVL available from Pharmacia; and pEF1/V5, pcDNA3.1, and pRc/CMV2 available from Invitrogen. Other suitable vectors will be readily apparent

5 to the skilled artisan.

Any strong promoter known to those skilled in the art can be used for driving the expression of polynucleotide sequence of the invention. Suitable promoters include adenoviral promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus (CMV) promoter; the 10 respiratory syncytial virus (RSV) promoter; inducible promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoAI promoter; human globin promoters; viral thymidine kinase promoters, such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs; the b-actin promoter; and human growth hormone promoters. The promoter also may be the 15 native promoter for the polynucleotides of the invention.

Unlike other gene therapy techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired 20 polypeptide for periods of up to six months.

The polynucleotide construct of the invention can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, 25 pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular, fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma 30 of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non- 35 differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. In vivo muscle cells are particularly competent in their

5 ability to take up and express polynucleotides.

For the naked nucleic acid sequence injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 mg/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, 10 as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration.

The preferred route of administration is by the parenteral route of injection 15 into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked DNA constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

20 The naked polynucleotides are delivered by any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, and so-called "gene guns". These delivery methods are known in the art.

The constructs may also be delivered with delivery vehicles such as viral 25 sequences, viral particles, liposome formulations, lipofectin, precipitating agents, etc. Such methods of delivery are known in the art.

In certain embodiments, the polynucleotide constructs of the invention are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and 30 neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner et al., Proc. Natl. Acad. Sci. USA , 84:7413-7416 (1987), which is herein incorporated by reference); mRNA (Malone et 35 al., Proc. Natl. Acad. Sci. USA , 86:6077-6081 (1989), which is herein incorporated by reference); and purified transcription factors (Debs et al., J. Biol. Chem.,

5 265:10189-10192 (1990), which is herein incorporated by reference), in functional  
form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleyloxy]propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand  
10 Island, N.Y. (See, also, Felgner et al., Proc. Natl. Acad. Sci. USA, 84:7413-7416 (1987), which is herein incorporated by reference). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).

Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication NO: WO 90/11092  
15 (which is herein incorporated by reference) for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., Felgner et al., Proc. Natl. Acad. Sci. USA, 84:7413-7417, which is herein incorporated by reference. Similar methods can be used to prepare liposomes from other cationic lipid materials.

20 Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE),  
25 among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

For example, commercially dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine  
30 (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and is hydrated the following day with deionized water. The sample is then sonicated for 2  
35 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at

5 15EC. Alternatively, negatively charged vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred. 10 The various liposome-nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger et al., *Methods of Immunology*, 101:512-527 (1983), which is herein incorporated by reference. For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass 15 tube and subsequently hydrating with a solution of the material to be encapsulated. SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as 20 sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods 25 include Ca<sup>2+</sup>-EDTA chelation (Papahadjopoulos et al., *Biochim. Biophys. Acta*, 394:483 (1975); Wilson et al., *Cell*, 17:77 (1979)); ether injection (Deamer et al., *Biochim. Biophys. Acta*, 443:629 (1976); Ostro et al., *Biochem. Biophys. Res. Commun.*, 76:836 (1977); Fraley et al., *Proc. Natl. Acad. Sci. USA*, 76:3348 (1979)); detergent dialysis (Enoch et al., *Proc. Natl. Acad. Sci. USA*, 76:145 (1979)); and 30 reverse-phase evaporation (REV) (Fraley et al., *J. Biol. Chem.*, 255:10431 (1980); Szoka et al., *Proc. Natl. Acad. Sci. USA*, 75:145 (1978); Schaefer-Ridder et al., *Science*, 215:166 (1982)), which are herein incorporated by reference.

Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ratio will be from about 5:1 to about 1:5. More preferably, the 35 ratio will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

U.S. Patent NO: 5,676,954 (which is herein incorporated by reference) reports

5 on the injection of genetic material, complexed with cationic liposomes carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication NO: WO 94/9469 (which are herein incorporated by reference) provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 10 5,580,859, 5,703,055, and international publication NO: WO 94/9469 (which are herein incorporated by reference) provide methods for delivering DNA-cationic lipid complexes to mammals.

In certain embodiments, cells are engineered, ex vivo or in vivo, using a retroviral particle containing RNA which comprises a sequence encoding 15 polypeptides of the invention. Retroviruses from which the retroviral plasmid vectors may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, Rous sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

20 The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PE501, PA317, R-2, R-AM, PA12, T19-14X, VT-19-17-H2, RCRE, RCRIP, GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human Gene Therapy , 1:5-14 (1990), which is incorporated herein by 25 reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO4 precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then administered to a host.

30 The producer cell line generates infectious retroviral vector particles which include polynucleotide encoding polypeptides of the invention. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either in vitro or in vivo. The transduced eukaryotic cells will express polypeptides of the invention.

In certain other embodiments, cells are engineered, ex vivo or in vivo, with 35 polynucleotides of the invention contained in an adenovirus vector. Adenovirus can be manipulated such that it encodes and expresses polypeptides of the invention, and

5 at the same time is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. Adenovirus expression is achieved without integration of the viral DNA into the host cell chromosome, thereby alleviating concerns about insertional mutagenesis. Furthermore, adenoviruses have been used as live enteric vaccines for many years with an excellent safety profile (Schwartzenbacher et al., Am. Rev. Respir. Dis., 10 109:233-238 (1974)). Finally, adenovirus mediated gene transfer has been demonstrated in a number of instances including transfer of alpha-1-antitrypsin and CFTR to the lungs of cotton rats (Rosenfeld et al., Science, 252:431-434 (1991); Rosenfeld et al., Cell, 68:143-155 (1992)). Furthermore, extensive studies to attempt to establish adenovirus as a causative agent in human cancer were uniformly negative 15 (Green et al. Proc. Natl. Acad. Sci. USA, 76:6606 (1979)).

Suitable adenoviral vectors useful in the present invention are described, for example, in Kozarsky and Wilson, Curr. Opin. Genet. Devel., 3:499-503 (1993); Rosenfeld et al., Cell, 68:143-155 (1992); Engelhardt et al., Human Genet. Ther., 4:759-769 (1993); Yang et al., Nature Genet., 7:362-369 (1994); Wilson et al., Nature 20, 365:691-692 (1993); and U.S. Patent NO: 5,652,224, which are herein incorporated by reference. For example, the adenovirus vector Ad2 is useful and can be grown in human 293 cells. These cells contain the E1 region of adenovirus and constitutively express E1a and E1b, which complement the defective adenoviruses by providing the products of the genes deleted from the vector. In addition to Ad2, other varieties of adenovirus (e.g., Ad3, Ad5, and Ad7) are also useful in the present invention. 25

Preferably, the adenoviruses used in the present invention are replication deficient. Replication deficient adenoviruses require the aid of a helper virus and/or packaging cell line to form infectious particles. The resulting virus is capable of infecting cells and can express a polynucleotide of interest which is operably linked to 30 a promoter, but cannot replicate in most cells. Replication deficient adenoviruses may be deleted in one or more of all or a portion of the following genes: E1a, E1b, E3, E4, E2a, or L1 through L5.

In certain other embodiments, the cells are engineered, *ex vivo* or *in vivo*, using an adeno-associated virus (AAV). AAVs are naturally occurring defective 35 viruses that require helper viruses to produce infectious particles (Muzyczka, Curr. Topics in Microbiol. Immunol., 158:97 (1992)). It is also one of the few viruses that

5 may integrate its DNA into non-dividing cells. Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate, but space for exogenous DNA is limited to about 4.5 kb. Methods for producing and using such AAVs are known in the art. See, for example, U.S. Patent Nos. 5,139,941, 5,173,414, 5,354,678, 5,436,146, 5,474,935, 5,478,745, and 5,589,377.

10 For example, an appropriate AAV vector for use in the present invention will include all the sequences necessary for DNA replication, encapsidation, and host-cell integration. The polynucleotide construct containing polynucleotides of the invention is inserted into the AAV vector using standard cloning methods, such as those found in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor 15 Press (1989). The recombinant AAV vector is then transfected into packaging cells which are infected with a helper virus, using any standard technique, including lipofection, electroporation, calcium phosphate precipitation, etc. Appropriate helper viruses include adenoviruses, cytomegaloviruses, vaccinia viruses, or herpes viruses. Once the packaging cells are transfected and infected, they will produce infectious 20 AAV viral particles which contain the polynucleotide construct of the invention. These viral particles are then used to transduce eukaryotic cells, either ex vivo or in vivo. The transduced cells will contain the polynucleotide construct integrated into its genome, and will express the desired gene product.

Another method of gene therapy involves operably associating heterologous 25 control regions and endogenous polynucleotide sequences (e.g. encoding the polypeptide sequence of interest) via homologous recombination (see, e.g., U.S. Patent NO: 5,641,670, issued June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA, 30 86:8932-8935 (1989); and Zijlstra et al., Nature, 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not normally expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made, using standard techniques known in the art, which contain the promoter with targeting sequences flanking the promoter. 35 Suitable promoters are described herein. The targeting sequence is sufficiently complementary to an endogenous sequence to permit homologous recombination of

5 the promoter-targeting sequence with the endogenous sequence. The targeting sequence will be sufficiently near the 5' end of the desired endogenous polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination.

The promoter and the targeting sequences can be amplified using PCR.  
10 Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter. The amplified promoter and targeting sequences are digested and  
15 ligated together.

The promoter-targeting sequence construct is delivered to the cells, either as naked polynucleotide, or in conjunction with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, whole viruses, lipofection, precipitating agents, etc., described in more detail above. The P promoter-targeting sequence can  
20 be delivered by any method, included direct needle injection, intravenous injection, topical administration, catheter infusion, particle accelerators, etc. The methods are described in more detail below.

The promoter-targeting sequence construct is taken up by cells. Homologous recombination between the construct and the endogenous sequence takes place, such  
25 that an endogenous sequence is placed under the control of the promoter. The promoter then drives the expression of the endogenous sequence.

The polynucleotides encoding polypeptides of the present invention may be administered along with other polynucleotides encoding angiogenic proteins. Angiogenic proteins include, but are not limited to, acidic and basic fibroblast growth  
30 factors, VEGF-1, VEGF-2 (VEGF-C), VEGF-3 (VEGF-B), epidermal growth factor alpha and beta, platelet-derived endothelial cell growth factor, platelet-derived growth factor, tumor necrosis factor alpha, hepatocyte growth factor, insulin like growth factor, colony stimulating factor, macrophage colony stimulating factor, granulocyte/macrophage colony stimulating factor, and nitric oxide synthase.

35 Preferably, the polynucleotide encoding a polypeptide of the invention contains a secretory signal sequence that facilitates secretion of the protein. Typically,

5 the signal sequence is positioned in the coding region of the polynucleotide to be expressed towards or at the 5' end of the coding region. The signal sequence may be homologous or heterologous to the polynucleotide of interest and may be homologous or heterologous to the cells to be transfected. Additionally, the signal sequence may be chemically synthesized using methods known in the art.

10 Any mode of administration of any of the above-described polynucleotides constructs can be used so long as the mode results in the expression of one or more molecules in an amount sufficient to provide a therapeutic effect. This includes direct needle injection, systemic injection, catheter infusion, biolistic injectors, particle accelerators (i.e., "gene guns"), gelfoam sponge depots, other commercially available  
15 depot materials, osmotic pumps (e.g., Alza minipumps), oral or suppositorial solid (tablet or pill) pharmaceutical formulations, and decanting or topical applications during surgery. For example, direct injection of naked calcium phosphate-precipitated plasmid into rat liver and rat spleen or a protein-coated plasmid into the portal vein has resulted in gene expression of the foreign gene in the rat livers. (Kaneda et al.,  
20 *Science*, 243:375 (1989)).

A preferred method of local administration is by direct injection. Preferably, a recombinant molecule of the present invention complexed with a delivery vehicle is administered by direct injection into or locally within the area of arteries. Administration of a composition locally within the area of arteries refers to injecting  
25 the composition centimeters and preferably, millimeters within arteries.

Another method of local administration is to contact a polynucleotide construct of the present invention in or around a surgical wound. For example, a patient can undergo surgery and the polynucleotide construct can be coated on the surface of tissue inside the wound or the construct can be injected into areas of tissue  
30 inside the wound.

Therapeutic compositions useful in systemic administration, include recombinant molecules of the present invention complexed to a targeted delivery vehicle of the present invention. Suitable delivery vehicles for use with systemic administration comprise liposomes comprising ligands for targeting the vehicle to a  
35 particular site.

Preferred methods of systemic administration, include intravenous injection,

5 aerosol, oral and percutaneous (topical) delivery. Intravenous injections can be performed using methods standard in the art. Aerosol delivery can also be performed using methods standard in the art (see, for example, Stribling et al., Proc. Natl. Acad. Sci. USA , 89:11277-11281 (1992), which is incorporated herein by reference). Oral delivery can be performed by complexing a polynucleotide construct of the present  
10 invention to a carrier capable of withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers, include plastic capsules or tablets, such as those known in the art. Topical delivery can be performed by mixing a polynucleotide construct of the present invention with a lipophilic reagent (e.g., DMSO) that is capable of passing into the skin.

15 Determining an effective amount of substance to be delivered can depend upon a number of factors including, for example, the chemical structure and biological activity of the substance, the age and weight of the animal, the precise condition requiring treatment and its severity, and the route of administration. The frequency of treatments depends upon a number of factors, such as the amount of  
20 polynucleotide constructs administered per dose, as well as the health and history of the subject. The precise amount, number of doses, and timing of doses will be determined by the attending physician or veterinarian. Therapeutic compositions of the present invention can be administered to any animal, preferably to mammals and birds. Preferred mammals include humans, dogs, cats, mice, rats, rabbits sheep, cattle,  
25 horses and pigs, with humans being particularly preferred.

### **Biological Activities**

The polynucleotides or polypeptides, or agonists or antagonists of the present invention can be used in assays to test for one or more biological activities. If these  
30 polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides or polypeptides, or agonists or antagonists could be used to treat the associated disease.

### **35 Cardiovascular Disorders**

Polynucleotides or polypeptides, or agonists or antagonists of the invention

5 may be used to treat, prevent, and/or diagnose cardiovascular diseases, disorders, and/or conditions, including peripheral artery disease, such as limb ischemia.

Cardiovascular diseases, disorders, and/or conditions include cardiovascular abnormalities, such as arterio-arterial fistula, arteriovenous fistula, cerebral arteriovenous malformations, congenital heart defects, pulmonary atresia, and 10 Scimitar Syndrome. Congenital heart defects include aortic coarctation, cor triatriatum, coronary vessel anomalies, crisscross heart, dextrocardia, patent ductus arteriosus, Ebstein's anomaly, Eisenmenger complex, hypoplastic left heart syndrome, levocardia, tetralogy of fallot, transposition of great vessels, double outlet right ventricle, tricuspid atresia, persistent truncus arteriosus, and heart septal defects, such 15 as aortopulmonary septal defect, endocardial cushion defects, Lutembacher's Syndrome, trilogy of Fallot, ventricular heart septal defects.

Cardiovascular diseases, disorders, and/or conditions also include heart disease, such as arrhythmias, carcinoid heart disease, high cardiac output, low cardiac output, cardiac tamponade, endocarditis (including bacterial), heart aneurysm, cardiac 20 arrest, congestive heart failure, congestive cardiomyopathy, paroxysmal dyspnea, cardiac edema, heart hypertrophy, congestive cardiomyopathy, left ventricular hypertrophy, right ventricular hypertrophy, post-infarction heart rupture, ventricular septal rupture, heart valve diseases, myocardial diseases, myocardial ischemia, pericardial effusion, pericarditis (including constrictive and tuberculous), 25 pneumopericardium, postpericardiotomy syndrome, pulmonary heart disease, rheumatic heart disease, ventricular dysfunction, hyperemia, cardiovascular pregnancy complications, Scimitar Syndrome, cardiovascular syphilis, and cardiovascular tuberculosis.

Arrhythmias include sinus arrhythmia, atrial fibrillation, atrial flutter, 30 bradycardia, extrasystole, Adams-Stokes Syndrome, bundle-branch block, sinoatrial block, long QT syndrome, parasystole, Lown-Ganong-Levine Syndrome, Mahaim-type pre-excitation syndrome, Wolff-Parkinson-White syndrome, sick sinus syndrome, tachycardias, and ventricular fibrillation. Tachycardias include paroxysmal tachycardia, supraventricular tachycardia, accelerated idioventricular rhythm, 35 atrioventricular nodal reentry tachycardia, ectopic atrial tachycardia, ectopic junctional tachycardia, sinoatrial nodal reentry tachycardia, sinus tachycardia,

5 Torsades de Pointes, and ventricular tachycardia.

Heart valve disease include aortic valve insufficiency, aortic valve stenosis, heart murmurs, aortic valve prolapse, mitral valve prolapse, tricuspid valve prolapse, mitral valve insufficiency, mitral valve stenosis, pulmonary atresia, pulmonary valve insufficiency, pulmonary valve stenosis, tricuspid atresia, tricuspid valve insufficiency, and tricuspid valve stenosis.

10 Myocardial diseases include alcoholic cardiomyopathy, congestive cardiomyopathy, hypertrophic cardiomyopathy, aortic subvalvular stenosis, pulmonary subvalvular stenosis, restrictive cardiomyopathy, Chagas cardiomyopathy, endocardial fibroelastosis, endomyocardial fibrosis, Kearns Syndrome, myocardial reperfusion injury, and myocarditis.

15 Myocardial ischemias include coronary disease, such as angina pectoris, coronary aneurysm, coronary arteriosclerosis, coronary thrombosis, coronary vasospasm, myocardial infarction and myocardial stunning.

20 Cardiovascular diseases also include vascular diseases such as aneurysms, angiodysplasia, angiomas, bacillary angiomas, Hippel-Lindau Disease, Klippel-Trenaunay-Weber Syndrome, Sturge-Weber Syndrome, angioneurotic edema, aortic diseases, Takayasu's Arteritis, aortitis, Leriche's Syndrome, arterial occlusive diseases, arteritis, enarteritis, polyarteritis nodosa, cerebrovascular diseases, disorders, and/or conditions, diabetic angiopathies, diabetic retinopathy, embolisms, thrombosis, 25 erythromelalgia, hemorrhoids, hepatic veno-occlusive disease, hypertension, hypotension, ischemia, peripheral vascular diseases, phlebitis, pulmonary veno-occlusive disease, Raynaud's disease, CREST syndrome, retinal vein occlusion, Scimitar syndrome, superior vena cava syndrome, telangiectasia, atacia telangiectasia, hereditary hemorrhagic telangiectasia, varicocele, varicose veins, varicose ulcer, 30 vasculitis, and venous insufficiency.

Aneurysms include dissecting aneurysms, false aneurysms, infected aneurysms, ruptured aneurysms, aortic aneurysms, cerebral aneurysms, coronary aneurysms, heart aneurysms, and iliac aneurysms.

35 Arterial occlusive diseases include arteriosclerosis, intermittent claudication, carotid stenosis, fibromuscular dysplasias, mesenteric vascular occlusion, Moyamoya disease, renal artery obstruction, retinal artery occlusion, and thromboangiitis

5 obliterans.

Cerebrovascular diseases, disorders, and/or conditions include carotid artery diseases, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformation, cerebral artery diseases, cerebral embolism and thrombosis, carotid artery thrombosis, sinus thrombosis, 10 Wallenberg's syndrome, cerebral hemorrhage, epidural hematoma, subdural hematoma, subarachnoid hemorrhage, cerebral infarction, cerebral ischemia (including transient), subclavian steal syndrome, periventricular leukomalacia, vascular headache, cluster headache, migraine, and vertebrobasilar insufficiency.

Embolisms include air embolisms, amniotic fluid embolisms, cholesterol 15 embolisms, blue toe syndrome, fat embolisms, pulmonary embolisms, and thromboembolisms. Thrombosis include coronary thrombosis, hepatic vein thrombosis, retinal vein occlusion, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, and thrombophlebitis.

Ischemia includes cerebral ischemia, ischemic colitis, compartment 20 syndromes, anterior compartment syndrome, myocardial ischemia, reperfusion injuries, and peripheral limb ischemia. Vasculitis includes aortitis, arteritis, Behcet's Syndrome, Churg-Strauss Syndrome, mucocutaneous lymph node syndrome, thromboangiitis obliterans, hypersensitivity vasculitis, Schoenlein-Henoch purpura, allergic cutaneous vasculitis, and Wegener's granulomatosis.

25 Polynucleotides or polypeptides, or agonists or antagonists of the invention, are especially effective for the treatment of critical limb ischemia and coronary disease.

Polypeptides may be administered using any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous 30 injection, topical administration, catheter infusion, biostatic injectors, particle accelerators, gelfoam sponge depots, other commercially available depot materials, osmotic pumps, oral or suppositorial solid pharmaceutical formulations, decanting or topical applications during surgery, aerosol delivery. Such methods are known in the art. Polypeptides of the invention may be administered as part of a Therapeutic, 35 described in more detail below. Methods of delivering polynucleotides of the invention are described in more detail herein.

### Diseases at the Cellular Level

Diseases associated with increased cell survival or the inhibition of apoptosis that could be treated, prevented, and/or diagnosed by the polynucleotides or polypeptides and/or antagonists or agonists of the invention, include cancers (such as 10 follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, including, but not limited to colon cancer, cardiac tumors, pancreatic cancer, melanoma, retinoblastoma, glioblastoma, lung cancer, intestinal cancer, testicular cancer, stomach cancer, neuroblastoma, myxoma, myoma, lymphoma, endothelioma, osteoblastoma, osteoclastoma, osteosarcoma, chondrosarcoma, adenoma, breast 15 cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer); autoimmune diseases, disorders, and/or conditions (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and 20 adenoviruses), inflammation, graft v. host disease, acute graft rejection, and chronic graft rejection. In preferred embodiments, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention are used to inhibit growth, progression, and/or metastasis of cancers, in particular those listed above.

Additional diseases or conditions associated with increased cell survival that 25 could be treated, prevented or diagnosed by the polynucleotides or polypeptides, or agonists or antagonists of the invention, include, but are not limited to, progression, and/or metastases of malignancies and related disorders such as leukemia (including acute leukemias (e.g., acute lymphocytic leukemia, acute myelocytic leukemia (including myeloblastic, promyelocytic, myelomonocytic, monocytic, and 30 erythroleukemia)) and chronic leukemias (e.g., chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia)), polycythemia vera, lymphomas (e.g., Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors including, but not limited to, sarcomas and carcinomas such as fibrosarcoma, myxosarcoma, liposarcoma, 35 chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma,

5 Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct 10 carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendrogioma, menangioma, melanoma, neuroblastoma, and retinoblastoma.

15 Diseases associated with increased apoptosis that could be treated, prevented, and/or diagnosed by the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, include AIDS; neurodegenerative diseases, disorders, and/or conditions (such as Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration and brain tumor or 20 prior associated disease); autoimmune diseases, disorders, and/or conditions (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) myelodysplastic syndromes (such as aplastic anemia), graft v. host disease, ischemic injury (such as 25 that caused by myocardial infarction, stroke and reperfusion injury), liver injury (e.g., hepatitis related liver injury, ischemia/reperfusion injury, cholestosis (bile duct injury) and liver cancer); toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia.

30 **Wound Healing and Epithelial Cell Proliferation**

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, for therapeutic purposes, for example, to stimulate epithelial cell proliferation and basal keratinocytes for the purpose of wound healing, 35 and to stimulate hair follicle production and healing of dermal wounds. Polynucleotides or polypeptides, as well as agonists or antagonists of the invention,

5 may be clinically useful in stimulating wound healing including surgical wounds, excisional wounds, deep wounds involving damage of the dermis and epidermis, eye tissue wounds, dental tissue wounds, oral cavity wounds, diabetic ulcers, dermal ulcers, cubitus ulcers, arterial ulcers, venous stasis ulcers, burns resulting from heat exposure or chemicals, and other abnormal wound healing conditions such as uremia,  
10 malnutrition, vitamin deficiencies and complications associated with systemic treatment with steroids, radiation therapy and antineoplastic drugs and antimetabolites. Polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to promote dermal reestablishment subsequent to dermal loss

The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to increase the adherence of skin grafts to a wound bed and to stimulate re-epithelialization from the wound bed. The following are a non-exhaustive list of grafts that polynucleotides or polypeptides, agonists or antagonists of the invention, could be used to increase adherence to a wound bed: autografts, artificial skin, allografts, autodermic graft, autoepidermic grafts, avascular grafts,  
20 Blair-Brown grafts, bone graft, braphoplastic grafts, cutis graft, delayed graft, dermic graft, epidermic graft, fascia graft, full thickness graft, heterologous graft, xenograft, homologous graft, hyperplastic graft, lamellar graft, mesh graft, mucosal graft, Ollier-Thiersch graft, omenpal graft, patch graft, pedicle graft, penetrating graft, split skin graft, thick split graft. The polynucleotides or polypeptides, and/or agonists or  
25 antagonists of the invention, can be used to promote skin strength and to improve the appearance of aged skin.

It is believed that the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, will also produce changes in hepatocyte proliferation, and epithelial cell proliferation in the lung, breast, pancreas, stomach, small intestine, and large intestine. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could promote proliferation of epithelial cells such as sebocytes, hair follicles, hepatocytes, type II pneumocytes, mucin-producing goblet cells, and other epithelial cells and their progenitors contained within the skin, lung, liver, and gastrointestinal tract. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, may promote proliferation of endothelial cells, keratinocytes, and basal keratinocytes.

5 The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could also be used to reduce the side effects of gut toxicity that result from radiation, chemotherapy treatments or viral infections. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, may have a cytoprotective effect on the small intestine mucosa. The polynucleotides or 10 polypeptides, and/or agonists or antagonists of the invention, may also stimulate healing of mucositis (mouth ulcers) that result from chemotherapy and viral infections.

15 The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could further be used in full regeneration of skin in full and partial thickness skin defects, including burns, (i.e., repopulation of hair follicles, sweat glands, and sebaceous glands), treatment of other skin defects such as psoriasis. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to treat epidermolysis bullosa, a defect in adherence of the epidermis to the underlying dermis which results in frequent, open and painful blisters by accelerating 20 reepithelialization of these lesions. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could also be used to treat gastric and duodenal ulcers and help heal by scar formation of the mucosal lining and regeneration of glandular mucosa and duodenal mucosal lining more rapidly. Inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis, are 25 diseases which result in destruction of the mucosal surface of the small or large intestine, respectively. Thus, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to promote the resurfacing of the mucosal surface to aid more rapid healing and to prevent progression of inflammatory bowel disease. Treatment with the polynucleotides or polypeptides, and/or agonists or 30 antagonists of the invention, is expected to have a significant effect on the production of mucus throughout the gastrointestinal tract and could be used to protect the intestinal mucosa from injurious substances that are ingested or following surgery. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to treat diseases associate with the under expression of the 35 polynucleotides of the invention.

Moreover, the polynucleotides or polypeptides, and/or agonists or antagonists

5 of the invention, could be used to prevent and heal damage to the lungs due to various pathological states. A growth factor such as the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, which could stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent or treat acute or chronic lung damage. For example, emphysema, which  
10 results in the progressive loss of aveoli, and inhalation injuries, i.e., resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli could be effectively treated, prevented, and/or diagnosed using the polynucleotides or polypeptides, and/or agonists or antagonists of the invention. Also, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention,  
15 could be used to stimulate the proliferation of and differentiation of type II pneumocytes, which may help treat or prevent disease such as hyaline membrane diseases, such as infant respiratory distress syndrome and bronchopulmonary displasia, in premature infants.

20 The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could stimulate the proliferation and differentiation of hepatocytes and, thus, could be used to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances (i.e., acetaminophen, carbon tetrachloride and other hepatotoxins known in the art).

25 In addition, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used treat or prevent the onset of diabetes mellitus. In patients with newly diagnosed Types I and II diabetes, where some islet cell function remains, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to maintain the islet function so as to alleviate, delay or  
30 prevent permanent manifestation of the disease. Also, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used as an auxiliary in islet cell transplantation to improve or promote islet cell function.

### Neurological Diseases

35 Nervous system diseases, disorders, and/or conditions, which can be treated, prevented, and/or diagnosed with the compositions of the invention (e.g.,

5 polypeptides, polynucleotides, and/or agonists or antagonists), include, but are not limited to, nervous system injuries, and diseases, disorders, and/or conditions which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated, prevented, and/or diagnosed in a patient (including human and non-human mammalian patients)

10 according to the invention, include but are not limited to, the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems: (1) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia; (2) traumatic lesions, including lesions caused by physical

15 injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries; (3) malignant lesions, in which a portion of the nervous system is destroyed or injured by malignant tissue which is either a nervous system associated malignancy or a malignancy derived from non-nervous system tissue; (4) infectious lesions, in which a portion of the nervous system is

20 destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis; (5) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease,

25 Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis (ALS); (6) lesions associated with nutritional diseases, disorders, and/or conditions, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami

30 disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration; (7) neurological lesions associated with systemic diseases including, but not limited to, diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis; (8) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and (9) demyelinated lesions in

35 which a portion of the nervous system is destroyed or injured by a demyelinating disease including, but not limited to, multiple sclerosis, human immunodeficiency

5 virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

In a preferred embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the invention are used to protect neural cells from the damaging effects of cerebral hypoxia. According to this embodiment, the compositions of the invention  
10 are used to treat, prevent, and/or diagnose neural cell injury associated with cerebral hypoxia. In one aspect of this embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose neural cell injury associated with cerebral ischemia. In another aspect of this embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the  
15 invention are used to treat, prevent, and/or diagnose neural cell injury associated with cerebral infarction. In another aspect of this embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose or prevent neural cell injury associated with a stroke. In a further aspect of this embodiment, the polypeptides, polynucleotides, or agonists or  
20 antagonists of the invention are used to treat, prevent, and/or diagnose neural cell injury associated with a heart attack.

The compositions of the invention which are useful for treating or preventing a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of  
25 limitation, compositions of the invention which elicit any of the following effects may be useful according to the invention: (1) increased survival time of neurons in culture; (2) increased sprouting of neurons in culture or in vivo; (3) increased production of a neuron-associated molecule in culture or in vivo, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or (4) decreased symptoms of  
30 neuron dysfunction in vivo. Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may routinely be measured using a method set forth herein or otherwise known in the art, such as, for example, the method set forth in Arakawa et al. (J. Neurosci. 10:3507-3515 (1990)); increased sprouting of neurons may be detected by methods known in  
35 the art, such as, for example, the methods set forth in Pestronk et al. (Exp. Neurol. 70:65-82 (1980)) or Brown et al. (Ann. Rev. Neurosci. 4:17-42 (1981)); increased

5 production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., using techniques known in the art and depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

10 In specific embodiments, motor neuron diseases, disorders, and/or conditions that may be treated, prevented, and/or diagnosed according to the invention include, but are not limited to, diseases, disorders, and/or conditions such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as diseases, disorders, and/or conditions that selectively affect neurons such as amyotrophic lateral sclerosis, and including, but not limited to, progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary

15 20 Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

### **Infectious Disease**

A polypeptide or polynucleotide and/or agonist or antagonist of the present invention can be used to treat, prevent, and/or diagnose infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated, prevented, and/or diagnosed. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, polypeptide or polynucleotide and/or agonist or antagonist of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated, prevented, and/or diagnosed by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention. Examples of viruses, include, but are not limited to Examples of viruses, include, but are not limited to the following DNA and RNA viruses and viral families: Arbovirus,

5 Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Dengue, EBV, HIV, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza A, Influenza B, and parainfluenza), Papiloma virus,  
10 Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, respiratory syncytial virus, encephalitis, eye infections (e.g., conjunctivitis, keratitis),  
15 chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), Japanese B encephalitis, Junin, Chikungunya, Rift Valley fever, yellow fever, meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts),  
20 and viremia. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat, prevent, and/or diagnose any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose: meningitis, Dengue, EBV, and/or hepatitis (e.g., hepatitis B). In an additional specific  
25 embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat patients nonresponsive to one or more other commercially available hepatitis vaccines. In a further specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose AIDS.  
30 Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated, prevented, and/or diagnosed by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, include, but not limited to, the following Gram-Negative and Gram-positive bacteria and bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Nocardia), Cryptococcus neoformans, Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia  
35

5 (e.g., *Borrelia burgdorferi*), Brucellosis, Candidiasis, *Campylobacter*,  
Coccidioidomycosis, Cryptococcosis, Dermatocycoses, *E. coli* (e.g., Enterotoxigenic  
*E. coli* and Enterohemorrhagic *E. coli*), Enterobacteriaceae (*Klebsiella*, *Salmonella*  
(e.g., *Salmonella typhi*, and *Salmonella paratyphi*), *Serratia*, *Yersinia*), *Erysipelothrix*,  
*Helicobacter*, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales,  
10 *Mycobacterium leprae*, *Vibrio cholerae*, Neisseriaceae (e.g., *Acinetobacter*,  
*Gonorrhea*, *Menigococcal*), *Meisseria meningitidis*, Pasteurellacea Infections (e.g.,  
*Actinobacillus*, *Heamophilus* (e.g., *Heamophilus influenza type B*), *Pasteurella*),  
*Pseudomonas*, Rickettsiaceae, Chlamydiaceae, Syphilis, *Shigella* spp.,  
Staphylococcal, Meningiococcal, Pneumococcal and Streptococcal (e.g.,  
15 *Streptococcus pneumoniae* and Group B *Streptococcus*). These bacterial or fungal  
families can cause the following diseases or symptoms, including, but not limited to:  
bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis),  
gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia,  
prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as  
20 Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease,  
Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea,  
meningitis (e.g., mengitis types A and B), Chlamydia, Syphilis, Diphtheria, Leprosy,  
Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo,  
Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g.,  
25 cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections.  
Polynucleotides or polypeptides, agonists or antagonists of the invention, can be used  
to treat, prevent, and/or diagnose any of these symptoms or diseases. In specific  
embodiments, polynucleotides, polypeptides, agonists or antagonists of the invention  
are used to treat, prevent, and/or diagnose: tetanus, Diphteria, botulism, and/or  
30 meningitis type B.

Moreover, parasitic agents causing disease or symptoms that can be treated,  
prevented, and/or diagnosed by a polynucleotide or polypeptide and/or agonist or  
antagonist of the present invention include, but not limited to, the following families  
or class: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis,  
35 Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis,  
Toxoplasmosis, Trypanosomiasis, and Trichomonas and Sporozoans (e.g.,

5 Plasmodium virax, Plasmodium falciparum, Plasmodium malariae and Plasmodium ovale). These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), malaria, pregnancy complications, and toxoplasmosis. polynucleotides or  
10 polypeptides, or agonists or antagonists of the invention, can be used to treat, prevent, and/or diagnose any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose malaria.

Preferably, treatment or prevention using a polypeptide or polynucleotide  
15 and/or agonist or antagonist of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a  
20 vaccine to raise an immune response against infectious disease.

### Binding Activity

A polypeptide of the present invention may be used to screen for molecules  
25 that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the  
30 polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can  
35 be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate

5 cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of  
10 either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

15 Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a  
20 standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

25 Additionally, the receptor to which a polypeptide of the invention binds can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting (Coligan, et al., *Current Protocols in Immun.*, 1(2), Chapter 5, (1991)). For example, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the polypeptides, for  
30 example, NIH3T3 cells which are known to contain multiple receptors for the FGF family proteins, and SC-3 cells, and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are exposed to the polypeptide of the present invention, after they have been labeled. The polypeptides  
35 can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase.

5 Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clones that encodes the putative receptor.

As an alternative approach for receptor identification, the labeled polypeptides  
10 can be photoaffinity linked with cell membrane or extract preparations that express  
the receptor molecule. Cross-linked material is resolved by PAGE analysis and  
exposed to X-ray film. The labeled complex containing the receptors of the  
polypeptides can be excised, resolved into peptide fragments, and subjected to protein  
microsequencing. The amino acid sequence obtained from microsequencing would be  
15 used to design a set of degenerate oligonucleotide probes to screen a cDNA library to  
identify the genes encoding the putative receptors.

Moreover, the techniques of gene-shuffling, motif-shuffling, exon-shuffling,  
and/or codon-shuffling (collectively referred to as "DNA shuffling") may be  
employed to modulate the activities of polypeptides of the invention thereby  
20 effectively generating agonists and antagonists of polypeptides of the invention. See  
generally, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and  
5,837,458, and Patten, P. A., et al., *Curr. Opinion Biotechnol.* 8:724-33 (1997);  
Harayama, S. *Trends Biotechnol.* 16(2):76-82 (1998); Hansson, L. O., et al., *J. Mol.*  
*Biol.* 287:265-76 (1999); and Lorenzo, M. M. and Blasco, R. *Biotechniques*  
25 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated  
by reference). In one embodiment, alteration of polynucleotides and corresponding  
polypeptides of the invention may be achieved by DNA shuffling. DNA shuffling  
involves the assembly of two or more DNA segments into a desired polynucleotide  
sequence of the invention molecule by homologous, or site-specific, recombination.  
30 In another embodiment, polynucleotides and corresponding polypeptides of the  
invention may be altered by being subjected to random mutagenesis by error-prone  
PCR, random nucleotide insertion or other methods prior to recombination. In another  
embodiment, one or more components, motifs, sections, parts, domains, fragments,  
etc., of the polypeptides of the invention may be recombined with one or more  
35 components, motifs, sections, parts, domains, fragments, etc. of one or more  
heterologous molecules. In preferred embodiments, the heterologous molecules are

5 family members. In further preferred embodiments, the heterologous molecule is a growth factor such as, for example, platelet-derived growth factor (PDGF), insulin-like growth factor (IGF-I), transforming growth factor (TGF)-alpha, epidermal growth factor (EGF), fibroblast growth factor (FGF), TGF-beta, bone morphogenetic protein (BMP)-2, BMP-4, BMP-5, BMP-6, BMP-7, activins A and B, decapentaplegic(dpp),  
10 60A, OP-2, dorsalin, growth differentiation factors (GDFs), nodal, MIS, inhibin-alpha, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta5, and glial-derived neurotrophic factor (GDNF).

15 Other preferred fragments are biologically active fragments of the polypeptides of the invention. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

20 Additionally, this invention provides a method of screening compounds to identify those which modulate the action of the polypeptide of the present invention.  
25 An example of such an assay comprises combining a mammalian fibroblast cell, a the polypeptide of the present invention, the compound to be screened and 3[H] thymidine under cell culture conditions where the fibroblast cell would normally proliferate. A control assay may be performed in the absence of the compound to be screened and compared to the amount of fibroblast proliferation in the presence of the compound to determine if the compound stimulates proliferation by determining the uptake of 3[H] thymidine in each case. The amount of fibroblast cell proliferation is measured by liquid scintillation chromatography which measures the incorporation of 3[H] thymidine. Both agonist and antagonist compounds may be identified by this procedure.

30 In another method, a mammalian cell or membrane preparation expressing a receptor for a polypeptide of the present invention is incubated with a labeled polypeptide of the present invention in the presence of the compound. The ability of the compound to enhance or block this interaction could then be measured. Alternatively, the response of a known second messenger system following 35 interaction of a compound to be screened and the receptor is measured and the ability of the compound to bind to the receptor and elicit a second messenger response is

5 measured to determine if the compound is a potential agonist or antagonist. Such second messenger systems include but are not limited to, cAMP guanylate cyclase, ion channels or phosphoinositide hydrolysis.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat, prevent, and/or diagnose  
10 disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptides of the invention from suitably manipulated cells or tissues. Therefore, the invention includes a method of identifying compounds which bind to the polypeptides of the invention  
15 comprising the steps of: (a) incubating a candidate binding compound with the polypeptide; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with the polypeptide, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been  
20 altered.

Also, one could identify molecules bind a polypeptide of the invention experimentally by using the beta-pleated sheet regions contained in the polypeptide sequence of the protein. Accordingly, specific embodiments of the invention are directed to polynucleotides encoding polypeptides which comprise, or alternatively consist of, the amino acid sequence of each beta pleated sheet regions in a disclosed polypeptide sequence. Additional embodiments of the invention are directed to polynucleotides encoding polypeptides which comprise, or alternatively consist of, any combination or all of contained in the polypeptide sequences of the invention. Additional preferred embodiments of the invention are directed to polypeptides which  
25 comprise, or alternatively consist of, the amino acid sequence of each of the beta pleated sheet regions in one of the polypeptide sequences of the invention. Additional embodiments of the invention are directed to polypeptides which comprise, or alternatively consist of, any combination or all of the beta pleated sheet regions in one of the polypeptide sequences of the invention.

5 **Targeted Delivery**

In another embodiment, the invention provides a method of delivering compositions to targeted cells expressing a receptor for a polypeptide of the invention, or cells expressing a cell bound form of a polypeptide of the invention.

As discussed herein, polypeptides or antibodies of the invention may be 10 associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (including antibodies) that are associated with heterologous polypeptides or nucleic 15 acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

20 In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention (e.g., polypeptides of the invention or antibodies of the invention) in association with toxins or cytotoxic prodrugs.

By "toxin" is meant compounds that bind and activate endogenous cytotoxic 25 effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing 30 containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. By "cytotoxic prodrug" is meant a non-toxic compound that is converted by an enzyme, normally present in the cell, into 35 a cytotoxic compound. Cytotoxic prodrugs that may be used according to the methods of the invention include, but are not limited to, glutamyl derivatives of benzoic acid

5 mustard alkylating agent, phosphate derivatives of etoposide or mitomycin C, cytosine arabinoside, daunorubisin, and phenoxyacetamide derivatives of doxorubicin.

### Drug Screening

10 Further contemplated is the use of the polypeptides of the present invention, or the polynucleotides encoding these polypeptides, to screen for molecules which modify the activities of the polypeptides of the present invention. Such a method would include contacting the polypeptide of the present invention with a selected compound(s) suspected of having antagonist or agonist activity, and assaying the 15 activity of these polypeptides following binding.

This invention is particularly useful for screening therapeutic compounds by using the polypeptides of the present invention, or binding fragments thereof, in any of a variety of drug screening techniques. The polypeptide or fragment employed in such a test may be affixed to a solid support, expressed on a cell surface, free in 20 solution, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. One may measure, for example, the formulation of complexes between the agent being tested and a polypeptide of the present 25 invention.

Thus, the present invention provides methods of screening for drugs or any other agents which affect activities mediated by the polypeptides of the present invention. These methods comprise contacting such an agent with a polypeptide of the present invention or a fragment thereof and assaying for the presence of a complex 30 between the agent and the polypeptide or a fragment thereof, by methods well known in the art. In such a competitive binding assay, the agents to screen are typically labeled. Following incubation, free agent is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of a particular agent to bind to the polypeptides of the present invention.

35 Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the polypeptides of the present

5 invention, and is described in great detail in European Patent Application 84/03564, published on September 13, 1984, which is incorporated herein by reference herein. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with polypeptides of the present invention and  
10 washed. Bound polypeptides are then detected by methods well known in the art. Purified polypeptides are coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies may be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays  
15 in which neutralizing antibodies capable of binding polypeptides of the present invention specifically compete with a test compound for binding to the polypeptides or fragments thereof. In this manner, the antibodies are used to detect the presence of any peptide which shares one or more antigenic epitopes with a polypeptide of the invention.

20 The human HGPR4 polypeptides and/or peptides of the present invention, or immunogenic fragments or oligopeptides thereof, can be used for screening therapeutic drugs or compounds in a variety of drug screening techniques. The fragment employed in such a screening assay may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The reduction or  
25 abolition of activity of the formation of binding complexes between the ion channel protein and the agent being tested can be measured. Thus, the present invention provides a method for screening or assessing a plurality of compounds for their specific binding affinity with a HGPR4 polypeptide, or a bindable peptide fragment, of this invention, comprising providing a plurality of compounds, combining the  
30 HGPR4 polypeptide, or a bindable peptide fragment, with each of a plurality of compounds for a time sufficient to allow binding under suitable conditions and detecting binding of the HGPR4 polypeptide or peptide to each of the plurality of test

5 compounds, thereby identifying the compounds that specifically bind to the HGPR4 polypeptide or peptide.

Methods of identifying compounds that modulate the activity of the novel human HGPR4 polypeptides and/or peptides are provided by the present invention and comprise combining a potential or candidate compound or drug modulator of 10 glycine receptor biological activity with an HGPR4 polypeptide or peptide, for example, the HGPR4 amino acid sequence as set forth in SEQ ID NO:2, and measuring an effect of the candidate compound or drug modulator on the biological activity of the HGPR4 polypeptide or peptide. Such measurable effects include, for example, physical binding interaction; the ability to cleave a suitable glycine receptor substrate; effects on native and cloned HGPR4-expressing cell line; and effects of 15 modulators or other glycine receptor-mediated physiological measures.

Another method of identifying compounds that modulate the biological activity of the novel HGPR4 polypeptides of the present invention comprises combining a potential or candidate compound or drug modulator of a glycine receptor 20 biological activity with a host cell that expresses the HGPR4 polypeptide and measuring an effect of the candidate compound or drug modulator on the biological activity of the HGPR4 polypeptide. The host cell can also be capable of being induced to express the HGPR4 polypeptide, e.g., via inducible expression. Physiological effects of a given modulator candidate on the HGPR4 polypeptide can 25 also be measured. Thus, cellular assays for particular glycine receptor modulators may be either direct measurement or quantification of the physical biological activity of the HGPR4 polypeptide, or they may be measurement or quantification of a physiological effect. Such methods preferably employ a HGPR4 polypeptide as described herein, or an overexpressed recombinant HGPR4 polypeptide in suitable 30 host cells containing an expression vector as described herein, wherein the HGPR4 polypeptide is expressed, overexpressed, or undergoes upregulated expression.

Another aspect of the present invention embraces a method of screening for a compound that is capable of modulating the biological activity of a HGPR4 polypeptide, comprising providing a host cell containing an expression vector 35 harboring a nucleic acid sequence encoding a HGPR4 polypeptide, or a functional peptide or portion thereof (e.g., SEQ ID NOS:2); determining the biological activity

5 of the expressed HGPR4 polypeptide in the absence of a modulator compound; contacting the cell with the modulator compound and determining the biological activity of the expressed HGPR4 polypeptide in the presence of the modulator compound. In such a method, a difference between the activity of the HGPR4 polypeptide in the presence of the modulator compound and in the absence of the 10 modulator compound indicates a modulating effect of the compound.

Essentially any chemical compound can be employed as a potential modulator or ligand in the assays according to the present invention. Compounds tested as glycine receptor modulators can be any small chemical compound, or biological entity (e.g., protein, sugar, nucleic acid, lipid). Test compounds will typically be small 15 chemical molecules and peptides. Generally, the compounds used as potential modulators can be dissolved in aqueous or organic (e.g., DMSO-based) solutions. The assays are designed to screen large chemical libraries by automating the assay steps and providing compounds from any convenient source. Assays are typically run in parallel, for example, in microtiter formats on microtiter plates in robotic assays. 20 There are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland), for example. Also, compounds may be synthesized by methods known in the art.

High throughput screening methodologies are particularly envisioned for the 25 detection of modulators of the novel HGPR4 polynucleotides and polypeptides described herein. Such high throughput screening methods typically involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (e.g., ligand or modulator compounds). Such combinatorial chemical libraries or ligand libraries are then screened in one or more 30 assays to identify those library members (e.g., particular chemical species or subclasses) that display a desired characteristic activity. The compounds so identified can serve as conventional lead compounds, or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical 35 compounds generated either by chemical synthesis or biological synthesis, by combining a number of chemical building blocks (i.e., reagents such as amino acids).

5 As an example, a linear combinatorial library, e.g., a polypeptide or peptide library, is formed by combining a set of chemical building blocks in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide or peptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

10 The preparation and screening of combinatorial chemical libraries is well known to those having skill in the pertinent art. Combinatorial libraries include, without limitation, peptide libraries (e.g. U.S. Patent No. 5,010,175; Furka, 1991, *Int. J. Pept. Prot. Res.*, 37:487-493; and Houghton et al., 1991, *Nature*, 354:84-88). Other chemistries for generating chemical diversity libraries can also be used. Nonlimiting 15 examples of chemical diversity library chemistries include, peptoids (PCT Publication No. WO 91/019735), encoded peptides (PCT Publication No. WO 93/20242), random bio-oligomers (PCT Publication No. WO 92/00091), benzodiazepines (U.S. Patent No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs et al., 1993, *Proc. Natl. Acad. Sci. USA*, 90:6909-6913), vinylogous 20 polypeptides (Hagihara et al., 1992, *J. Amer. Chem. Soc.*, 114:6568), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann et al., 1992, *J. Amer. Chem. Soc.*, 114:9217-9218), analogous organic synthesis of small compound libraries (Chen et al., 1994, *J. Amer. Chem. Soc.*, 116:2661), oligocarbamates (Cho et al., 1993, *Science*, 261:1303), and/or peptidyl phosphonates (Campbell et al., 1994, *J. Org. 25 Chem.*, 59:658), nucleic acid libraries (see Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent No. 5,539,083), antibody libraries (e.g., Vaughn et al., 1996, *Nature Biotechnology*, 14(3):309-314) and PCT/US96/10287), carbohydrate libraries (e.g., Liang et al., 1996, *Science*, 274:1520-1522) and U.S. Patent No. 5,593,853), small organic molecule libraries (e.g., benzodiazepines, Baum 30 C&EN, Jan. 18, 1993, page 33; and U.S. Patent No. 5,288,514; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; and the like).

Devices for the preparation of combinatorial libraries are commercially 35 available (e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050

5 Plus, Millipore, Bedford, MA). In addition, a large number of combinatorial libraries are commercially available (e.g., ComGenex, Princeton, NJ; Asinex, Moscow, Russia; Tripos, Inc., St. Louis, MO; ChemStar, Ltd., Moscow, Russia; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD, and the like).

In one embodiment, the invention provides solid phase based *in vitro* assays in  
10 a high throughput format, where the cell or tissue expressing an ion channel is attached to a solid phase substrate. In such high throughput assays, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to perform a separate assay against a selected potential modulator, or, if concentration or incubation time effects  
15 are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 96 modulators. If 1536 well plates are used, then a single plate can easily assay from about 100 to about 1500 different compounds. It is possible to assay several different plates per day; thus, for example, assay screens for up to about 6,000-20,000 different compounds are possible using the  
20 described integrated systems.

In another of its aspects, the present invention encompasses screening and small molecule (e.g., drug) detection assays which involve the detection or identification of small molecules that can bind to a given protein, i.e., a HGPR4 polypeptide or peptide. Particularly preferred are assays suitable for high throughput  
25 screening methodologies.

In such binding-based detection, identification, or screening assays, a functional assay is not typically required. All that is needed is a target protein, preferably substantially purified, and a library or panel of compounds (e.g., ligands, drugs, small molecules) or biological entities to be screened or assayed for binding to  
30 the protein target. Preferably, most small molecules that bind to the target protein will modulate activity in some manner, due to preferential, higher affinity binding to functional areas or sites on the protein.

An example of such an assay is the fluorescence based thermal shift assay (3-Dimensional Pharmaceuticals, Inc., 3DP, Exton, PA) as described in U.S. Patent Nos.  
35 6,020,141 and 6,036,920 to Pantoliano et al.; see also, J. Zimmerman, 2000, *Gen. Eng. News*, 20(8)). The assay allows the detection of small molecules (e.g., drugs,

5 ligands) that bind to expressed, and preferably purified, ion channel polypeptide based on affinity of binding determinations by analyzing thermal unfolding curves of protein-drug or ligand complexes. The drugs or binding molecules determined by this technique can be further assayed, if desired, by methods, such as those described herein, to determine if the molecules affect or modulate function or activity of the  
10 target protein.

To purify a HGPR4 polypeptide or peptide to measure a biological binding or ligand binding activity, the source may be a whole cell lysate that can be prepared by successive freeze-thaw cycles (e.g., one to three) in the presence of standard protease inhibitors. The HGPR4 polypeptide may be partially or completely purified by  
15 standard protein purification methods, e.g., affinity chromatography using specific antibody described *infra*, or by ligands specific for an epitope tag engineered into the recombinant HGPR4 polypeptide molecule, also as described herein. Binding activity can then be measured as described.

Compounds which are identified according to the methods provided herein,  
20 and which modulate or regulate the biological activity or physiology of the HGPR4 polypeptides according to the present invention are a preferred embodiment of this invention. It is contemplated that such modulatory compounds may be employed in treatment and therapeutic methods for treating a condition that is mediated by the novel HGPR4 polypeptides by administering to an individual in need of such  
25 treatment a therapeutically effective amount of the compound identified by the methods described herein.

In addition, the present invention provides methods for treating an individual in need of such treatment for a disease, disorder, or condition that is mediated by the HGPR4 polypeptides of the invention, comprising administering to the individual a  
30 therapeutically effective amount of the HGPR4-modulating compound identified by a method provided herein.

#### Antisense And Ribozyme (Antagonists)

In specific embodiments, antagonists according to the present invention are  
35 nucleic acids corresponding to the sequences contained in SEQ ID NO:X, or the complementary strand thereof, and/or to nucleotide sequences contained a deposited

5 clone. In one embodiment, antisense sequence is generated internally by the organism, in another embodiment, the antisense sequence is separately administered (see, for example, O'Connor, *Neurochem.*, 56:560 (1991). Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Antisense technology can be used to control gene expression through antisense DNA or RNA, or  
10 through triple-helix formation. Antisense techniques are discussed for example, in Okano, *Neurochem.*, 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance, Lee et al., *Nucleic Acids Research*, 6:3073 (1979); Cooney et al., *Science*, 241:456 (1988); and Dervan et al., *Science*, 251:1300 (1991). The  
15 methods are based on binding of a polynucleotide to a complementary DNA or RNA.

For example, the use of c-myc and c-myb antisense RNA constructs to inhibit the growth of the non-lymphocytic leukemia cell line HL-60 and other cell lines was previously described. (Wickstrom et al. (1988); Anfossi et al. (1989)). These experiments were performed in vitro by incubating cells with the oligoribonucleotide.  
20 A similar procedure for in vivo use is described in WO 91/15580. Briefly, a pair of oligonucleotides for a given antisense RNA is produced as follows: A sequence complimentary to the first 15 bases of the open reading frame is flanked by an EcoR1 site on the 5' end and a HindIII site on the 3' end. Next, the pair of oligonucleotides is heated at 90°C for one minute and then annealed in 2X ligation buffer (20mM TRIS  
25 HCl pH 7.5, 10mM MgCl<sub>2</sub>, 10MM dithiothreitol (DTT) and 0.2 mM ATP) and then ligated to the EcoR1/Hind III site of the retroviral vector PMV7 (WO 91/15580).

For example, the 5' coding portion of a polynucleotide that encodes the mature polypeptide of the present invention may be used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is  
30 designed to be complementary to a region of the gene involved in transcription thereby preventing transcription and the production of the receptor. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into receptor polypeptide.

In one embodiment, the antisense nucleic acid of the invention is produced  
35 intracellularly by transcription from an exogenous sequence. For example, a vector or a portion thereof, is transcribed, producing an antisense nucleic acid (RNA) of the

5 invention. Such a vector would contain a sequence encoding the antisense nucleic acid of the invention. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for 10 replication and expression in vertebrate cells. Expression of the sequence encoding a polypeptide of the invention, or fragments thereof, can be by any promoter known in the art to act in vertebrate, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, *Nature*, 29:304-310 (1981), the promoter contained in 15 the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., *Cell*, 22:787-797 (1980), the herpes thymidine promoter (Wagner et al., *Proc. Natl. Acad. Sci. U.S.A.*, 78:1441-1445 (1981), the regulatory sequences of the metallothionein gene (Brinster et al., *Nature*, 296:39-42 (1982)), etc.

20 The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a gene of interest. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double stranded antisense nucleic acids of the 25 invention, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the larger the hybridizing nucleic acid, the more base mismatches with a RNA sequence of the invention it may contain and still form a stable duplex (or triplex as the case may be). 30 One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

35 Oligonucleotides that are complementary to the 5' end of the message, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. See generally, Wagner, R., *Nature*, 372:333-335

5 (1994). Thus, oligonucleotides complementary to either the 5' - or 3' - non-translated, non-coding regions of a polynucleotide sequence of the invention could be used in an antisense approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides 10 complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5' -, 3' - or coding region of mRNA, antisense nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, 15 at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

The polynucleotides of the invention can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, 20 etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556 (1989); Lemaitre et al., Proc. Natl. Acad. Sci., 84:648-652 (1987); PCT Publication NO: WO88/09810, published December 15, 1988) or the blood-brain barrier (see, 25 e.g., PCT Publication NO: WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., BioTechniques, 6:958-976 (1988)) or intercalating agents. (See, e.g., Zon, Pharm. Res., 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, 30 etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including, but not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-35 carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-

5      methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiacytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-  
10     thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

15     The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

20     In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group including, but not limited to, a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

25     In yet another embodiment, the antisense oligonucleotide is an a-anomeric oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gautier et al., Nucl. Acids Res., 15:6625-6641 (1987)). The oligonucleotide is a 2-O-methylribonucleotide (Inoue et al., Nucl. Acids Res., 15:6131-6148 (1987)), or a chimeric RNA-DNA analogue (Inoue et al., FEBS Lett. 215:327-330 (1987)).

30     Polynucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (Nucl. Acids Res., 16:3209 (1988)), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., Proc. Natl. Acad. Sci. U.S.A., 85:7448-7451 (1988)), etc.

35     While antisense nucleotides complementary to the coding region sequence of the invention could be used, those complementary to the transcribed untranslated

5 region are most preferred.

Potential antagonists according to the invention also include catalytic RNA, or a ribozyme (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al, *Science*, 247:1222-1225 (1990). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy mRNAs corresponding to the polynucleotides of the invention, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5' -UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, *Nature*, 334:585-591 (1988). There are numerous potential hammerhead ribozyme cleavage sites within each nucleotide sequence disclosed in the sequence listing. Preferably, the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the mRNA corresponding to the polynucleotides of the invention; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

As in the antisense approach, the ribozymes of the invention can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express the polynucleotides of the invention *in vivo*. DNA constructs encoding the ribozyme may be introduced into the cell in the same manner as described above for the introduction of antisense encoding DNA. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive promoter, such as, for example, pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous messages and inhibit translation. Since ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Antagonist/agonist compounds may be employed to inhibit the cell growth and proliferation effects of the polypeptides of the present invention on neoplastic cells and tissues, i.e. stimulation of angiogenesis of tumors, and, therefore, retard or prevent abnormal cellular growth and proliferation, for example, in tumor formation

5 or growth.

The antagonist/agonist may also be employed to prevent hyper-vascular diseases, and prevent the proliferation of epithelial lens cells after extracapsular cataract surgery. Prevention of the mitogenic activity of the polypeptides of the present invention may also be desirous in cases such as restenosis after balloon 10 angioplasty.

The antagonist/agonist may also be employed to prevent the growth of scar tissue during wound healing.

The antagonist/agonist may also be employed to treat, prevent, and/or diagnose the diseases described herein.

15 Thus, the invention provides a method of treating or preventing diseases, disorders, and/or conditions, including but not limited to the diseases, disorders, and/or conditions listed throughout this application, associated with overexpression of a polynucleotide of the present invention by administering to a patient (a) an antisense molecule directed to the polynucleotide of the present invention, and/or (b) a 20 ribozyme directed to the polynucleotide of the present invention.

invention, and/or (b) a ribozyme directed to the polynucleotide of the present invention.

### Biotic Associations

25 A polynucleotide or polypeptide and/or agonist or antagonist of the present invention may increase the organisms ability, either directly or indirectly, to initiate and/or maintain biotic associations with other organisms. Such associations may be symbiotic, nonsymbiotic, endosymbiotic, macrosymbiotic, and/or microsymbiotic in nature. In general, a polynucleotide or polypeptide and/or agonist or antagonist of the 30 present invention may increase the organisms ability to form biotic associations with any member of the fungal, bacterial, lichen, mycorrhizal, cyanobacterial, dinoflagellate, and/or algal, kingdom, phylums, families, classes, genera, and/or species.

The mechanism by which a polynucleotide or polypeptide and/or agonist or 35 antagonist of the present invention may increase the host organisms ability, either directly or indirectly, to initiate and/or maintain biotic associations is variable, though

5 may include, modulating osmolarity to desirable levels for the symbiont, modulating pH to desirable levels for the symbiont, modulating secretions of organic acids, modulating the secretion of specific proteins, phenolic compounds, nutrients, or the increased expression of a protein required for host-biotic organisms interactions (e.g., a receptor, ligand, etc.). Additional mechanisms are known in the art and are  
10 encompassed by the invention (see, for example, "Microbial Signalling and Communication", eds., R. England, G. Hobbs, N. Bainton, and D. McL. Roberts, Cambridge University Press, Cambridge, (1999); which is hereby incorporated herein by reference).

In an alternative embodiment, a polynucleotide or polypeptide and/or agonist  
15 or antagonist of the present invention may decrease the host organisms ability to form biotic associations with another organism, either directly or indirectly. The mechanism by which a polynucleotide or polypeptide and/or agonist or antagonist of the present invention may decrease the host organisms ability, either directly or indirectly, to initiate and/or maintain biotic associations with another organism is  
20 variable, though may include, modulating osmolarity to undesirable levels, modulating pH to undesirable levels, modulating secretions of organic acids, modulating the secretion of specific proteins, phenolic compounds, nutrients, or the decreased expression of a protein required for host-biotic organisms interactions (e.g., a receptor, ligand, etc.). Additional mechanisms are known in the art and are  
25 encompassed by the invention (see, for example, "Microbial Signalling and Communication", eds., R. England, G. Hobbs, N. Bainton, and D. McL. Roberts, Cambridge University Press, Cambridge, (1999); which is hereby incorporated herein by reference).

The hosts ability to maintain biotic associations with a particular pathogen has  
30 significant implications for the overall health and fitness of the host. For example, human hosts have symbiosis with enteric bacteria in their gastrointestinal tracts, particularly in the small and large intestine. In fact, bacteria counts in feces of the distal colon often approach  $10^{12}$  per milliliter of feces. Examples of bowel flora in the gastrointestinal tract are members of the Enterobacteriaceae, Bacteriodes, in addition  
35 to a-hemolytic streptococci, E. coli, Bifobacteria, Anaerobic cocci, Eubacteria, Costridia, lactobacilli, and yeasts. Such bacteria, among other things, assist the host in

5 the assimilation of nutrients by breaking down food stuffs not typically broken down by the hosts digestive system, particularly in the hosts bowel. Therefore, increasing the hosts ability to maintain such a biotic association would help assure proper nutrition for the host.

10 Aberrations in the enteric bacterial population of mammals, particularly humans, has been associated with the following disorders: diarrhea, ileus, chronic inflammatory disease, bowel obstruction, duodenal diverticula, biliary calculous disease, and malnutrition. A polynucleotide or polypeptide and/or agonist or antagonist of the present invention are useful for treating, detecting, diagnosing, prognosing, and/or ameliorating, either directly or indirectly, and of the above 15 mentioned diseases and/or disorders associated with aberrant enteric flora population.

20 The composition of the intestinal flora, for example, is based upon a variety of factors, which include, but are not limited to, the age, race, diet, malnutrition, gastric acidity, bile salt excretion, gut motility, and immune mechanisms. As a result, the polynucleotides and polypeptides, including agonists, antagonists, and fragments thereof, may modulate the ability of a host to form biotic associations by affecting, 25 directly or indirectly, at least one or more of these factors.

25 Although the predominate intestinal flora comprises anaerobic organisms, an underlying percentage represents aerobes (e.g., *E. coli*). This is significant as such aerobes rapidly become the predominate organisms in intraabdominal infections – effectively becoming opportunistic early in infection pathogenesis. As a result, there is an intrinsic need to control aerobe populations, particularly for immune 30 compromised individuals.

30 In a preferred embodiment, a polynucleotides and polypeptides, including agonists, antagonists, and fragments thereof, are useful for inhibiting biotic associations with specific enteric symbiont organisms in an effort to control the population of such organisms.

35 Biotic associations occur not only in the gastrointestinal tract, but also on an in the integument. As opposed to the gastrointestinal flora, the cutaneous flora is comprised almost equally with aerobic and anaerobic organisms. Examples of cutaneous flora are members of the gram-positive cocci (e.g., *S. aureus*, coagulase-negative staphylococci, *micrococcus*, *M.sedentarius*), gram-positive bacilli (e.g.,

5 *Corynebacterium* species, *C. minutissimum*, *Brevibacterium* species, *Propoionibacterium* species, *P.acnes*), gram-negative bacilli (e.g., *Acinebacter* species), and fungi (*Pityrosporum orbiculare*). The relatively low number of flora associated with the integument is based upon the inability of many organisms to adhere to the skin. The organisms referenced above have acquired this unique ability.

10 Therefore, the polynucleotides and polypeptides of the present invention may have uses which include modulating the population of the cutaneous flora, either directly or indirectly.

Aberrations in the cutaneous flora are associated with a number of significant diseases and/or disorders, which include, but are not limited to the following: 15 impetigo, ecthyma, blistering distal dactulitis, pustules, folliculitis, cutaneous abscesses, pitted keratolysis, trichomycosis axillaris, dermatophytosis complex, axillary odor, erythrasma, cheesy foot odor, acne, tinea versicolor, seborrheic dermititis, and *Pityrosporum* folliculitis, to name a few. A polynucleotide or polypeptide and/or agonist or antagonist of the present invention are useful for 20 treating, detecting, diagnosing, prognosing, and/or ameliorating, either directly or indirectly, and of the above mentioned diseases and/or disorders associated with aberrant cutaneous flora population.

Additional biotic associations, including diseases and disorders associated with the aberrant growth of such associations, are known in the art and are 25 encompassed by the invention. See, for example, "Infectious Disease", Second Edition, Eds., S.L., Gorbach, J.G., Bartlett, and N.R., Blacklow, W.B. Saunders Company, Philadelphia, (1998); which is hereby incorporated herein by reference).

### Pheromones

30 In another embodiment, a polynucleotide or polypeptide and/or agonist or antagonist of the present invention may increase the organisms ability to synthesize, release, and/or respond to a pheromone, either directly or indirectly. Such a pheromone may, for example, alter the organisms behavior and/or metabolism.

35 A polynucleotide or polypeptide and/or agonist or antagonist of the present invention may modulate the biosynthesis and/or release of pheromones, the organisms ability to respond to pheromones (e.g., behaviorally, and/or metabolically), and/or the

5 organisms ability to detect pheromones, either directly or indirectly. Preferably, any of the pheromones, and/or volatiles released from the organism, or induced, by a polynucleotide or polypeptide and/or agonist or antagonist of the invention have behavioral effects on the organism.

For example, recent studies have shown that administration of picogram 10 quantities of androstadienone, the most prominent androstene present on male human axillary hair and on the male axillary skin, to the female vomeronasal organ resulted in a significant reduction of nervousness, tension and other negative feelings in the female recipients (Grosser-BI, et al., Psychoneuroendocrinology, 25(3): 289-99 (2000)).

15

### **Other Activities**

The polypeptide of the present invention, as a result of the ability to stimulate 20 vascular endothelial cell growth, may be employed in treatment for stimulating re-vascularization of ischemic tissues due to various disease conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions. These polypeptide may also be employed to stimulate angiogenesis and limb regeneration, as discussed above.

The polypeptide may also be employed for treating wounds due to injuries, 25 burns, post-operative tissue repair, and ulcers since they are mitogenic to various cells of different origins, such as fibroblast cells and skeletal muscle cells, and therefore, facilitate the repair or replacement of damaged or diseased tissue.

The polypeptide of the present invention may also be employed stimulate 30 neuronal growth and to treat, prevent, and/or diagnose neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions such as Alzheimer's disease, Parkinson's disease, and AIDS-related complex. The polypeptide of the invention may have the ability to stimulate chondrocyte growth, therefore, they may be employed to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts.

The polypeptide of the invention may also be employed to maintain organs 35 before transplantation or for supporting cell culture of primary tissues.

The polypeptide of the present invention may also be employed for

5 inducing tissue of mesodermal origin to differentiate in early embryos.

The polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

10 The polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, polypeptides or polynucleotides and/or agonist or antagonists of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, 15 utilization, and storage of energy.

20 Polypeptide or polynucleotides and/or agonist or antagonists of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression (including depressive diseases, disorders, and/or conditions), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

25 Polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also be used to increase the efficacy of a pharmaceutical composition, either directly or indirectly. Such a use may be administered in simultaneous conjunction with said pharmaceutical, or separately through either the same or different route of administration (e.g., intravenous for the polynucleotide or polypeptide of the present invention, and orally for the pharmaceutical, among others described herein.).

30 Polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also be used to prepare individuals for extraterrestrial travel, low gravity environments, prolonged exposure to extraterrestrial radiation levels, low oxygen levels, reduction of metabolic activity, exposure to extraterrestrial pathogens, etc. Such a use may be administered either prior to an extraterrestrial event, during an extraterrestrial event, or both. Moreover, such a use may result in a number of 35 beneficial changes in the recipient, such as, for example, any one of the following, non-limiting, effects: an increased level of hematopoietic cells, particularly red blood

5 cells which would aid the recipient in coping with low oxygen levels; an increased level of B-cells, T-cells, antigen presenting cells, and/or macrophages, which would aid the recipient in coping with exposure to extraterrestrial pathogens, for example; a temporary (i.e., reversible) inhibition of hematopoietic cell production which would aid the recipient in coping with exposure to extraterrestrial radiation levels; increase  
10 and/or stability of bone mass which would aid the recipient in coping with low gravity environments; and/or decreased metabolism which would effectively facilitate the recipients ability to prolong their extraterrestrial travel by any one of the following, non-limiting means: (i) aid the recipient by decreasing their basal daily energy requirements; (ii) effectively lower the level of oxidative and/or metabolic stress in  
15 recipient (i.e., to enable recipient to cope with increased extraterrestrial radiation levels by decreasing the level of internal oxidative/metabolic damage acquired during normal basal energy requirements; and/or (iii) enabling recipient to subsist at a lower metabolic temperature (i.e., cryogenic, and/or sub-cryogenic environment).

20 Polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

#### Other Preferred Embodiments

25 Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

30 Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the "5' NT of Start Codon of ORF" and ending with the nucleotide at about the position of the "3' NT of ORF" as defined for SEQ ID NO:X in Table 1.

35 Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

5 Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ 10 ID NO:X beginning with the nucleotide at about the position of the "5' NT of ORF" and ending with the nucleotide at about the position of the "3' NT of ORF" as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete 15 nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only 20 A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA 25 Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the 30 ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide 35 sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said cDNA clone.

5 A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said cDNA clone.

10 A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said cDNA clone.

15 A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one 20 nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

25 Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA 30 molecules.

35 A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by

5 a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least 10 one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a protein identified in Table 1, which method comprises a step of detecting in a biological 15 sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a cDNA clone identified by a cDNA Clone 20 Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 25 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said 30 panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone 35 in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

5 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

10 Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions "Total AA of the Open Reading Frame (ORF)" as set forth for SEQ ID NO:Y in Table 1.

15 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

20 Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

25 Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

30 Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

35 Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of the protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

40 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

45 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in

5 the amino acid sequence of the protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the protein encoded by a cDNA 10 clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group 15 consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a 20 polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the 25 deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino 30 acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at 35 least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in

5 Table 1; and a complete amino acid sequence of a protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide 10 molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected 15 from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

20 Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above 25 group.

Also preferred is a method for diagnosing a pathological condition associated with an organism with abnormal structure or expression of a gene encoding a protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid 30 sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a cDNA clone identified by a 35 cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

5 In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at 10 least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA 15 clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide 20 comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

25 Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule(s) into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

30 Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a protein comprising an amino acid sequence selected from the 35 group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the "Total AA of ORF" of SEQ ID NO:Y is

5 defined in Table 1; and an amino acid sequence of a protein encoded by a cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

10 Also preferred is a method of treatment of an individual in need of an increased level of a protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

15 Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

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Examples**Description of the Preferred Embodiments****Example 1 – Bioinformatics Analysis**

Ion channel sequences were used as probes to search the human genomic sequence database. The search program used was gapped BLAST (Altschul et al., 10 1997). Ion channel specific Hidden Markov Models (HMMs) built in-house or obtained from the public PFAM databases were also used as probes (Bateman et al., 2000). The search program used for HMMs was the Genewise/Wise2 package (http://www.sanger.ac.uk/Software/Wise2/index.shtml). The top genomic exon hits from the results were searched back against the non-redundant protein and patent 15 sequence databases. From this analysis BAC AL049610 was determined to possess a novel ion channel exon based on its homology to the putative human glycine receptor alpha 2 subunit (SEQ ID NO:13). The full length cDNA described herein as HGRA4 (SEQ ID NO:1, Figures 1A-C), was isolated using probes designed from the BAC AL049610 exon (SEQ ID NO:5). Based on this analysis, a partial sequence of the 20 novel human glycine receptor related gene, HGRA4, was identified. The full-length clone of this novel glycine receptor gene was experimentally obtained by using the sequence from genomic data.

Upon cloning the full-length HGRA4 polynucleotide, the clone corresponding to the HGRA4sv splice variant was obtained. The full-length sequence of the 25 HGRA4sv polynucleotide is provided in Figures 2A-B (SEQ ID NO:3).

**Example 2 - Method for Constructing a size fractionated brain cDNA Library**

Brain poly A + RNA was purchased from Clontech and converted into double 30 stranded cDNA using the SuperScript™ Plasmid System for cDNA Synthesis and Plasmid Cloning (Life Technologies) except that no radioisotope was incorporated in either of the cDNA synthesis steps and that the cDNA was fractionated by HPLC. This was accomplished on a TransGenomics HPLC system equipped with a size exclusion column (TosoHass) with dimensions of 7.8mm x 30cm and a particle size 35 of 10µm. Tris buffered saline was used as the mobile phase and the column was run at a flow rate of 0.5 mL/min.

5        The resulting chromatograms were analyzed to determine which fractions should be pooled to obtain the largest cDNA's; generally fractions that eluted in the range of 12 to 15 minutes were pooled. The cDNA was precipitated prior to ligation into the Sal I / Not I sites in the pSport vector supplied with the kit. Using a combination of PCR with primers to the ends of the vector and Sal I/Not I restriction  
10      enzyme digestion of mini-prep DNA, it was determined that the average insert size of the library was greater than 3.5 Kb. The overall complexity of the library was greater than  $10^7$  independent clones. The library was amplified in semi-solid agar for 2 days at 30° C. An aliquot (200 microliters) of the amplified library was inoculated into a 200 ml culture for single-stranded DNA isolation by super-infection with a f1 helper  
15      phage. After overnight growth, the released phage particles were precipitated with PEG and the DNA isolated with proteinase K, SDS and phenol extractions. The single stranded circular DNA was concentrated by ethanol precipitation and used for the cDNA capture experiments.

20      **Example 3 - Cloning of the Novel Human Glycine Receptor Alpha Subunit**

Using the predicted exon genomic sequence from bac AL049610, an antisense 80 bp oligo with biotin on the 5' end was designed with the following sequence;

5'-

25      bAGGGGCTGGAGGTTGGGACTATAAATGCCAGAACCTCCATTGGACCTCCATCTC  
TTGCCTGCAGGCAGTGGCCAAGC-3' (SEQ ID NO:6)

One microliter (one hundred and fifty nanograms) of the biotinylated oligo was added to six microliters (six micrograms) of a single-stranded covalently closed  
30      circular brain cDNA library (see Example 2) and seven microliters of 100% formamide in a 0.5 ml PCR tube. The mixture was heated in a thermal cycler to 95° C for 2 mins. Fourteen microliters of 2X hybridization buffer (50% formamide, 1.5 M NaCl, 0.04 M NaPO<sub>4</sub>, pH 7.2, 5 mM EDTA, 0.2% SDS) was added to the heated probe/cDNA library mixture and incubated at 42° C for 26 hours. Hybrids between  
35      the biotinylated oligo and the circular cDNA were isolated by diluting the hybridization mixture to 220 microliters in a solution containing 1 M NaCl, 10 mM

5 Tris-HCl pH 7.5, 1mM EDTA, pH 8.0 and adding 125 microliters of streptavidin magnetic beads. This solution was incubated at 42° C for 60 mins, mixing every 5 mins to resuspend the beads. The beads were separated from the solution with a magnet and the beads washed three times in 200 microliters of 0.1 X SSPE, 0.1% SDS at 45° C.

10 The single stranded cDNAs were release from the biotinlyated oligo/streptavidin magnetic bead complex by adding 50 microliters of 0.1 N NaOH and incubating at room temperature for 10 mins. Six microliters of 3 M Sodium Acetate was added along with 15 micrograms of glycogen and the solution ethanol precipitated with 120 microliters of 100% ethanol. The DNA was resuspend in 12 microliters of TE (10 mM Tris-HCl, pH 8.0), 1mM EDTA, and pH 8.0). The single stranded cDNA was converted into double strands in a thermal cycler by mixing 5 microliters of the captured DNA with 1.5 microliters 10 micromolar standard SP6 primer (homologous to a sequence on the cDNA cloning vector) and 1.5 microliters of 10 X PCR buffer. The mixture was heated to 95° C for 20 seconds, then ramped down 20 to 59 ° C. At this time 15 microliters of a repair mix, that was preheated to 70° C (Repair mix contains 4 microliters of 5 mM dNTPs (1.25 mM each), 1.5 microliters of 10X PCR buffer, 9.25 microliters of water, and 0.25 microliters of Taq polymerase). The solution was ramped back to 73° C and incubated for 23 mins. The repaired DNA was ethanol precipitate and resuspended in 10 microliters of TE. Two microliters 25 were electroporated in E. coli DH12S cells and resulting colonies were screen by PCR, using a primer pair designed from the genomic exonic sequence to identify the proper cDNAs.

Oligos used to identity the cDNA by PCR.

30

BAC2-10s TCGTTTCTATTCCTGGCT (SEQ ID NO:7)  
BAC2-10a CGGGAGATGGTGTCAATTCT (SEQ ID NO:8)

Those cDNA clones that were positive by PCR had the inserts sized and two clones were chosen for DNA sequencing. The clone E3 (HGRA4) and clone D8 (HGRA4sv) had several differences; 1) different sequences at their 5' end and the

5 presence of an alternatively spliced exon or unspliced intron that maintained the cDNAs coding potential. Both clones apparently were missing approximately 250 bp from their 5' ends. The nucleotide sequences for E3 and D8 were used to search all available databases using BLAST. An Incyte clone sequence (Incyte Clone No. G1934909) that overlapped E3 and D8 was identified that extended the 5' sequence to  
10 the putative initiating methionine.

**Example 4 – Expression profiling of novel human potassium channel modulatory beta subunit HGRA4**

The same PCR primer pair (SEQ ID NO:7 and 8) that was used to identify the  
15 HGRA4 cDNA clones was used to measure the steady state levels of mRNA by quantitative PCR. Briefly, first strand cDNA was made from commercially available mRNA. The relative amount of cDNA used in each assay was determined by performing a parallel experiment using a primer pair for a gene expressed in equal amounts in all tissues, cyclophilin. The cyclophilin primer pair detected small  
20 variations in the amount of cDNA in each sample and these data were used for normalization of the data obtained with the primer pair for HGRA4. The PCR data was converted into a relative assessment of the difference in transcript abundance amongst the tissues tested and the data is presented below. Transcripts corresponding to HGRA4 expressed highly in heart and colon; significantly in uterus, and to a lesser  
25 extent, in testis, and spinal cord.

**Example 5 – Method Of Assessing The Expression Profile Of The Novel HGPR4 Polypeptides Of The Present Invention Using Expanded mRNA Tissue and Cell Sources**

30 Total RNA from tissues was isolated using the Trizol protocol (Invitrogen) and quantified by determining its absorbance at 260nM. An assessment of the 18s and 28s ribosomal RNA bands was made by denaturing gel electrophoresis to determine RNA integrity.

35 The specific sequence to be measured was aligned with related genes found in GenBank to identity regions of significant sequence divergence to maximize primer and probe specificity. Gene-specific primers and probes were designed using the ABI

5 primer express software to amplify small amplicons (150 base pairs or less) to maximize the likelihood that the primers function at 100% efficiency. All primer/probe sequences were searched against Public Genbank databases to ensure target specificity. Primers and probes were obtained from ABI.

10 For HGPR4, the primer probe sequences were as follows

Forward Primer 5'- CCTTCCAGATCCACCTGAACCA -3' (SEQ ID NO:75)

Reverse Primer 5'- GATCCTGCCACCATGCTAGTTAA -3' (SEQ ID NO:76)

TaqMan Probe 5' - CTGGTCTCAGAAATATTCGTTCCGTTCCCT -3' (SEQ ID NO:77)

15

*DNA contamination*

To access the level of contaminating genomic DNA in the RNA, the RNA was divided into 2 aliquots and one half was treated with Rnase-free Dnase (Invitrogen).  
20 Samples from both the Dnase-treated and non-treated were then subjected to reverse transcription reactions with (RT+) and without (RT-) the presence of reverse transcriptase. TaqMan assays were carried out with gene-specific primers (see above) and the contribution of genomic DNA to the signal detected was evaluated by comparing the threshold cycles obtained with the RT+/RT- non-Dnase treated RNA to  
25 that on the RT+/RT- Dnase treated RNA. The amount of signal contributed by genomic DNA in the Dnased RT- RNA must be less than 10% of that obtained with Dnased RT+ RNA. If not the RNA was not used in actual experiments.

*Reverse Transcription reaction and Sequence Detection*

30 100ng of Dnase-treated total RNA was annealed to 2.5  $\mu$ M of the respective gene-specific reverse primer in the presence of 5.5 mM Magnesium Chloride by heating the sample to 72°C for 2 min and then cooling to 55° C for 30 min. 1.25 U/ $\mu$ l of MuLv reverse transcriptase and 500 $\mu$ M of each dNTP was added to the reaction and the tube was incubated at 37° C for 30 min. The sample was then heated to 90°C  
35 for 5 min to denature enzyme.

5 Quantitative sequence detection was carried out on an ABI PRISM 7700 by adding to the reverse transcribed reaction 2.5 $\mu$ M forward and reverse primers, 500 $\mu$ M of each dNTP, buffer and 5U AmpliTaq Gold<sup>TM</sup>. The PCR reaction was then held at 94°C for 12 min, followed by 40 cycles of 94° C for 15 sec and 60° C for 30 sec.

10 *Data handling*

The threshold cycle (C<sub>t</sub>) of the lowest expressing tissue (the highest C<sub>t</sub> value) was used as the baseline of expression and all other tissues were expressed as the relative abundance to that tissue by calculating the difference in C<sub>t</sub> value between the baseline and the other tissues and using it as the exponent in 2<sup>( $\Delta$ C<sub>t</sub>)</sup>

15 The expanded expression profile of the HGRA4 polypeptide, is provided in Figure 9 and described elsewhere herein.

**Example 6 – Assessing Ability Of HGRA4 Polypeptides To Function As Neurotransmission Inhibitors.**

20 To test for the ability of the newly describe proteins to function as inhibitors of neurotransmission, cDNAs representing full length versions of each of the splice forms (HGRA4 and HGRA4sv) can be transfected into a variety of cultured and primary cells types. For instance, HEK 293 cells expressing recombinant HGRA4 could be treated with glycine and chloride currents measured in both whole cell or 25 single channel recordings. The dose response curve for glycine could be determined and compared to that obtained when HGRA4 is co-expressed with vectors expressing a human glycine receptor beta subunit. A shift in responsiveness would suggest the two proteins were interacting in the classical pentameric 3:2 arrangement. These experiments could be repeated with other known agonists of the glycine receptor, 30 such beta-alanine as well as in the presence of known antagonist such as strychnine. Direct physical interaction between HGRA4 and other known glycine receptor subunits could be performed by using a variety of well known molecular biology techniques such as yeast 2-hybrid screens, and immunoprecipitations.

35 **Example 7 – Method of assessing ability of HGRA4 polypeptides to associate with glycine receptor subunits using the yeast two-hybrid system.**

5        In an effort to determine whether the HGRA4 polypeptides of the present invention are capable of functioning as glycine receptor alpha subunits, it would be important to effectively test the interaction between HGRA4 and various portions of other glycine receptor alpha or beta subunits, in a yeast two-hybrid system. Such a system could be created using methods known in the art (see, for example, S. Fields  
10 and O. Song, *Nature*, 340:245-246 (1989); and Gaston-SM and Loughlin-KR, *Urology*, 53(4): 835-42 (1999); which are hereby incorporated herein by reference in their entirety, including the articles referenced therein).

15        Cytoplasmic NH and COOH terminal domains of different glycine receptor alpha- or beta-subunits could be subcloned and expressed as fusion proteins of the  
15        GAL4 DNA binding (DB) domain using molecular biology techniques within the skill  
of the artisan.

20        Exemplary subunits which could be used in the two-hybrid system to assess HGRA4's ability to associate with other alpha or beta subunits include, but are not limited to, the NH and/or C-terminal domain of HGRA1, HGRA2, HGRA3, and the  
20        mouse GRA4.

**Example 8 – Method of assessing ability of HGRA4 polypeptides to form oligomeric complexes with itself or other glycine receptor subunits in solution.**

25        Aside from determining whether the HGRA4 polypeptides are capable of interacting with other glycine receptor alpha and/or beta subunits in a yeast two-hybrid assay, it would be an important next step to assess its ability to form oligomeric complexes with itself, in addition to other alpha or beta subunits in solution. Such a finding would be significant as it would provide convincing evidence  
30        that HGRA4 could serve as a glycine receptor alpha subunit and may modulate inhibitory neurotransmission function.

      A number of methods could be used to that are known in the art, for example, the method described by Sanguinetti, M.C., et al., *Nature*, 384:80-83 (1996) could be adapted using methods within the skill of the artisan.

5   **Example 9 – Method of assessing whether the formation of HGRA4/glycine receptor alpha subunits has any effect on inhibiting neurotransmission.**

Once the HGRA4 polypeptides are determined to form oligomeric and/or heteromultimeric complexes with other alpha or beta subunits, it would be important to determine whether such an interaction is physiologically relevant. Alternatively, 10 this experiment could be performed prior to the oligomerization and yeast-two hybrid experiments described above.

Expression constructs comprising the coding region of the HGRA4 polypeptide under the control of a constitutive or inducible promoter could be created and used to transiently or stably transfect a cell line lacking endogenous glycine 15 receptor alpha expression. Once transfected, the ability of the cells to transduce Cl- could be assessed using techniques known in the art. Alternatively, any cell line could be transfected with HGRA4 polypeptides and the glycine receptor function of the cell assessed. Alternatively, oocytes from the South African clawed frog *X. laevis* could be used to assess the ability of expressed HGRA4 polypeptides to modulate 20 endogenous or transfected neurotransmission function (for example, Wagner-CA; Friedrich-B; Setiawan-I; Lang-F; Broer, *Cell-Physiol-Biochem.*, 10(1-2):1-12 (2000); which is hereby incorporated herein by reference in its entirety, including the references cited therein). Additional methods could be applied for assessing the ability 25 of HGRA4 to modulate neurotransmission activity. For example, the method described by McDonald, T.V., et al., *Nature*, 388:289-292 (1997) could be adapted using methods within the skill of the artisan.

**Example 10 – Method of identifying the cognate ligand of the HGRA4 polypeptide.**

30   A number of methods are known in the art for identifying the cognate binding partner of a particular polypeptide. For example, the encoding HGRA4 polynucleotide could be engineered to comprise an epitope tag. The epitope could be any epitope known in the art or disclosed elsewhere herein. Once created, the epitope tagged HGRA4 encoding polynucleotide could be cloned into an expression vector and used 35 to transfect a variety of cell lines representing different tissue origins (e.g., brain, testis, etc.). The transfected cell lines could then be induced to overexpress the

5 HGRA4 polypeptide. Since other electrically silent channels appear to remain in the endoplasmic reticulum in the absence of their cognate binding partner, evidence for a cell type expressing the proper conducting channel would be the observed cell surface expression of HGRA4. The presence of the HGRA4 polypeptide on the cell surface could be determined by fractionating whole cell lysates into cellular and membrane  
10 protein fractions and performing immunoprecipitation using the antibody directed against the epitope engineered into the HGRA4 polypeptide. Monoclonal or polyclonal antibodies directed against the HGRA4 polypeptide could be created and used in place of the antibodies directed against the epitope.

Alternatively, the cell surface proteins could be distinguished from cellular  
15 proteins by biotinylating the surface proteins and then performing immunoprecipitations with antibody specific to the HGRA4 protein. After electrophoretic separation, the biotinylated protein could be detected with streptavidin-HRP (using standard methods known to those skilled in the art). Identification of the proteins bound to HGRA4 could be made in those cells by  
20 immunoprecipitation, followed by one-dimensional electrophoresis, followed by various versions of mass spectrometry. Such mass-spectrometry methods are known in the art, such as for example the methods taught by Ciphergen Biosystems Inc. (see US Patent No. 5,792,664; which is hereby incorporated herein by reference).

25 **Example 11 - Isolation of a Specific Clone from the Deposited Sample.**

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each  
30 cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 1-10 plasmid DNAs, each containing a different cDNA clone and/or partial cDNA clone; but such a deposit sample may include plasmids for more or less than 2 cDNA clones.

35 Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNA(s) cited for that clone in Table 1. First, a plasmid is directly

5 isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:1.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with 32P-( $\gamma$ -ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. 10 The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 15 1.104), or other techniques known to those of skill in the art. 20

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:1 (i.e., within the region of SEQ ID NO:1 bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain 25 reaction is carried out under routine conditions, for instance, in 25  $\mu$ l of reaction mixture with 0.5  $\mu$ g of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl<sub>2</sub>, 0.01% (w/v) gelatin, 20  $\mu$ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94 degree C for 1 min; annealing at 55 degree C for 1 min; elongation 30 at 72 degree C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

The polynucleotide(s) of the present invention, the polynucleotide encoding 35 the polypeptide of the present invention, or the polypeptide encoded by the deposited clone may represent partial, or incomplete versions of the complete coding region

5 (i.e., full-length gene). Several methods are known in the art for the identification of the 5' or 3' non-coding and/or coding portions of a gene which may not be present in the deposited clone. The methods that follow are exemplary and should not be construed as limiting the scope of the invention. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols 10 similar or identical to 5' and 3' "RACE" protocols that are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993)).

15 Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full-length gene.

20 This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA that may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to 25 remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

30 This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene. Moreover, it may be advantageous to optimize the RACE protocol to increase the probability of isolating 35 additional 5' or 3' coding or non-coding sequences. Various methods of optimizing a

5 RACE protocol are known in the art, though a detailed description summarizing these methods can be found in B.C. Schaefer, Anal. Biochem., 227:255-273, (1995).

An alternative method for carrying out 5' or 3' RACE for the identification of coding or non-coding sequences is provided by Frohman, M.A., et al., Proc.Nat'l.Acad.Sci.USA, 85:8998-9002 (1988). Briefly, a cDNA clone missing either 10 the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start of translation, therefor. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNAs reverse transcribed with 15 Superscript II (Gibco/BRL) and an antisense or I complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT 20 primer containing three adjacent restriction sites (XhoIJ Sail and Clal) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide- 25 agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or Sall, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with 30 the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from 35 Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-

5 stranded ligation to single-stranded cDNA), developed by Dumas et al., Nucleic Acids Res., 19:5227-32(1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to  
10 sequence past.

An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested  
15 cDNA-specific antisense primer and the plasmid-anchored primer.

*RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes*

Once a gene of interest is identified, several methods are available for the  
20 identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3'RACE. While the full-length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the  
25 existing sequence information from the original cDNA to generate the missing information. A method similar to 5'RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., Nucleic Acids Res., 21(7): 1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably 30 containing full-length gene RNA transcript and a primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A  
35 RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on

5 degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase if used is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA  
10 ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the apoptosis related of interest. The resultant product is then  
15 sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant apoptosis related.

**Example 12 - Tissue Distribution of Polypeptide.**

Tissue distribution of mRNA expression of polynucleotides of the present  
20 invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 11 is labeled with p32 using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN0-100 column (Clontech  
25 Laboratories, Inc.) according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various tissues for mRNA expression.

Tissue Northern blots containing the bound mRNA of various tissues are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech according to manufacturers protocol number PT1190-1. Northern blots  
30 can be produced using various protocols well known in the art (e.g., Sambrook et al). Following hybridization and washing, the blots are mounted and exposed to film at -70C overnight, and the films developed according to standard procedures.

**Example 13 - Chromosomal Mapping of the Polynucleotides.**

35 An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:1. This primer preferably spans about 100 nucleotides. This

5 primer set is then used in a polymerase chain reaction under the following set of conditions: 30 seconds, 95 degree C; 1 minute, 56 degree C; 1 minute, 70 degree C. This cycle is repeated 32 times followed by one 5 minute cycle at 70 degree C. Mammalian DNA, preferably human DNA, is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome 10 fragments (Bios, Inc). The reactions are analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

**Example 14 - Bacterial Expression of a Polypeptide.**

15 A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 11, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product 20 into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Ampr), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning 25 sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the *E. coli* strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, that 30 expresses the lacI repressor and also confers kanamycin resistance (Kanr). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid 35 culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The

5 cells are grown to an optical density 600 (O.D.600) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

10 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4 degree C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high 15 affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

20 Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

25 The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 30 4 degree C or frozen at -80 degree C.

#### **Example 15 - Purification of a Polypeptide from an Inclusion Body.**

35 The following alternative method can be used to purify a polypeptide expressed in E coli when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10 degree C.

5        Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10 degree C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution  
10      containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

15      The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M  
20      NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

25      The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4 degree C overnight to allow further GuHCl extraction.

30      Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4 degree C without mixing for 12 hours prior to further purification steps.

35      To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 um membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perceptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

40      Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perceptive Biosystems) and weak

5 anion (Poros CM-20, Perceptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under  
10 constant A280 monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Coomassie blue stained 16% SDS-PAGE gel when 5 ug of purified  
15 protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

**Example 16 - Cloning and Expression of a Polypeptide in a Baculovirus  
20 Expression System.**

In this example, the plasmid shuttle vector pAc373 is used to insert a polynucleotide into a baculovirus to express a polypeptide. A typical baculovirus expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction  
25 sites, which may include, for example BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is often used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene.  
30 The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pVL941 and pAcIM1, as one skilled in the art would readily appreciate, as long as  
35 the construct provides appropriately located signals for transcription, translation,

5 secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 11, to synthesize insertion fragments. The primers 10 used to amplify the cDNA insert should preferably contain restriction sites at the 5' end of the primers in order to clone the amplified product into the expression vector. Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified elsewhere herein (if applicable), is amplified using the PCR protocol described in Example 11. If 15 the naturally occurring signal sequence is used to produce the protein, the vector used does not need a second signal peptide. Alternatively, the vector can be modified to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 20 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

25 The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

30 The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA 35 sequencing.

5        Five ug of a plasmid containing the polynucleotide is co-transformed with 1.0 ug of a commercially available linearized baculovirus DNA ("BaculoGoldtm baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One ug of BaculoGoldtm virus DNA and 5ug of the plasmid are mixed in a sterile well of a  
10      microtiter plate containing 50ul of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 ul Lipofectin plus 90 ul Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is  
15      then incubated for 5 hours at 27 degrees C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27 degrees C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, supra. An agarose gel with "Blue Gal" (Life  
20      Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a  
25      micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 ul of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4 degree C.

30       To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine  
35      (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 uCi of 35S-methionine and 5 uCi 35S-cysteine (available from Amersham) are added. The cells

5 are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

10 Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

**Example 17 - Expression of a Polypeptide in Mammalian Cells.**

15 The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long 20 terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

25 Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

30 Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transformation with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transformed cells.

35 The transformed gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of

5 interest. (See, e.g., Alt, F. W., et al., *J. Biol. Chem.* 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., *Biochem. et Biophys. Acta*, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., *Biotechnology* 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., *Biochem J.* 227:277-279 (1991); Bebbington et al., *Bio/Technology* 10:169-175 (1992). Using these markers, the  
10 mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

A polynucleotide of the present invention is amplified according to the  
15 protocol outlined in herein. If the naturally occurring signal sequence is used to produce the protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.) The amplified fragment is isolated from a 1% agarose gel using a commercially available kit  
20 ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then  
25 transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transformation. Five  $\mu$ g of an expression plasmid is cotransformed with 0.5  $\mu$ g of the plasmid pSVneo using lipofectin (Felgner et al., supra). The plasmid pSV2-neo  
30 contains a dominant selectable marker, the neo gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml  
35 G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM,

5 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 uM, 2 uM, 5 uM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 uM. Expression of the desired gene product is analyzed, for instance, by SDS-  
10 PAGE and Western blot or by reversed phase HPLC analysis.

**Example 18 - Protein Fusions.**

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, 15 fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example described herein; see also EP A 394,827; Traunecker, et al., *Nature* 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the half-life time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a 20 specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying 25 the following protocol, which outlines the fusion of a polypeptide to an IgG molecule.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector. Note 30 that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

The naturally occurring signal sequence may be used to produce the protein (if applicable). Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 35 96/34891 and/or US Patent No. 6,066,781, *supra*.)

## 5 Human IgG Fc region:

GGGATCCGGAGCCAAATCTTCTGACAAAACTCACACATGCCACC  
GTGCCAGCACCTGAATCGAGGGTGCACCGTCAGTCTCCTCTCCCCC  
AAAACCCAAGGACACCCTCATGATCTCCGGACTCCTGAGGTACATGCG  
TGGTGGTGGACGTAAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC  
10 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC  
AGTACAACACAGCACGTACCGTGGTCAGCGTCCTCACCGTCTGCACCAAG  
GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGCCCT  
CCCAACCCCCATCGAGAAAACCATCTCAAAGCCAAGGGCAGCCCCGAG  
AACACAGGTGTACACCCCTGCCCATCCGGATGAGCTGACCAAGAAC  
15 CAGGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCAAGCGACATCGC  
CGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCACG  
CCTCCCGTGCTGGACTCCGACGGCTCCTCTCCTACAGCAAGCTCACC  
GTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCATGCTCCGTGAT  
GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCGTCTC  
20 CGGGTAAATGAGTGCACGGCCCGACTCTAGAGGAT (SEQ ID NO:37)

**Example 19 - Production of an Antibody from a Polypeptide.**

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing a polypeptide of the present invention are administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

30 In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., *Nature* 256:495 (1975); Köhler et al., *Eur. J. Immunol.* 6:511 (1976); Köhler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably,

5 with a polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56 degrees C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 ug/ml of streptomycin.

10 The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as 15 described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method 20 makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody that binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones that produce an antibody 25 whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')2 and other fragments of the 30 antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

35 For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using

5   genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 10 8702671; Boulianne et al., *Nature* 312:643 (1984); Neuberger et al., *Nature* 314:268 (1985).)

Moreover, in another preferred method, the antibodies directed against the polypeptides of the present invention may be produced in plants. Specific methods are disclosed in US Patent Nos. 5,959,177, and 6,080,560, which are hereby incorporated 15 in their entirety herein. The methods not only describe methods of expressing antibodies, but also the means of assembling foreign multimeric proteins in plants (i.e., antibodies, etc.), and the subsequent secretion of such antibodies from the plant.

**Example 20 - Regulation of Protein Expression Via Controlled Aggregation in 20 the Endoplasmic Reticulum.**

As described more particularly herein, proteins regulate diverse cellular processes in higher organisms, ranging from rapid metabolic changes to growth and differentiation. Increased production of specific proteins could be used to prevent certain diseases and/or disease states. Thus, the ability to modulate the expression of 25 specific proteins in an organism would provide significant benefits.

Numerous methods have been developed to date for introducing foreign genes, either under the control of an inducible, constitutively active, or endogenous promoter, into organisms. Of particular interest are the inducible promoters (see, M. Gossen, et al., *Proc. Natl. Acad. Sci. USA.*, 89:5547 (1992); Y. Wang, et al., *Proc. 30 Natl. Acad. Sci. USA*, 91:8180 (1994), D. No., et al., *Proc. Natl. Acad. Sci. USA*, 93:3346 (1996); and V.M. Rivera, et al., *Nature Med*, 2:1028 (1996); in addition to additional examples disclosed elsewhere herein). In one example, the gene for erythropoietin (Epo) was transferred into mice and primates under the control of a small molecule inducer for expression (e.g., tetracycline or rapamycin) (see, D. Bohl, 35 et al., *Blood*, 92:1512, (1998); K.G. Rendahl, et al., *Nat. Biotech*, 16:757, (1998); V.M. Rivera, et al., *Proc. Natl. Acad. Sci. USA*, 96:8657 (1999); and X.Ye et al.,

5     Science, 283:88 (1999). Although such systems enable efficient induction of the gene of interest in the organism upon addition of the inducing agent (i.e., tetracycline, rapamycin, etc.,), the levels of expression tend to peak at 24 hours and trail off to background levels after 4 to 14 days. Thus, controlled transient expression is virtually impossible using these systems, though such control would be desirable.

10    A new alternative method of controlling gene expression levels of a protein from a transgene (i.e., includes stable and transient transformants) has recently been elucidated (V.M. Rivera., et al., Science, 287:826-830, (2000)). This method does not control gene expression at the level of the mRNA like the aforementioned systems. Rather, the system controls the level of protein in an active secreted form. In the  
15    absence of the inducing agent, the protein aggregates in the ER and is not secreted. However, addition of the inducing agent results in dis-aggregation of the protein and the subsequent secretion from the ER. Such a system affords low basal secretion, rapid, high level secretion in the presence of the inducing agent, and rapid cessation of secretion upon removal of the inducing agent. In fact, protein secretion reached a  
20    maximum level within 30 minutes of induction, and a rapid cessation of secretion within 1 hour of removing the inducing agent. The method is also applicable for controlling the level of production for membrane proteins.

25    Detailed methods are presented in V.M. Rivera., et al., Science, 287:826-830, (2000)), briefly:

25    Fusion protein constructs are created using polynucleotide sequences of the present invention with one or more copies (preferably at least 2, 3, 4, or more) of a conditional aggregation domain (CAD) a domain that interacts with itself in a ligand-reversible manner (i.e., in the presence of an inducing agent) using molecular biology methods known in the art and discussed elsewhere herein. The CAD domain may be  
30    the mutant domain isolated from the human FKBP12 (Phe<sup>36</sup> to Met) protein (as disclosed in V.M. Rivera., et al., Science, 287:826-830, (2000), or alternatively other proteins having domains with similar ligand-reversible, self-aggregation properties. As a principle of design the fusion protein vector would contain a furin cleavage sequence operably linked between the polynucleotides of the present invention and  
35    the CAD domains. Such a cleavage site would enable the proteolytic cleavage of the CAD domains from the polypeptide of the present invention subsequent to secretion

5 from the ER and upon entry into the trans-Golgi (J.B. Denault, et al., FEBS Lett., 379:113, (1996)). Alternatively, the skilled artisan would recognize that any proteolytic cleavage sequence could be substituted for the furin sequence provided the substituted sequence is cleavable either endogenously (e.g., the furin sequence) or exogenously (e.g., post secretion, post purification, post production, etc.). The  
10 preferred sequence of each feature of the fusion protein construct, from the 5' to 3' direction with each feature being operably linked to the other, would be a promoter, signal sequence, "X" number of (CAD)x domains, the furin sequence (or other proteolytic sequence), and the coding sequence of the polypeptide of the present invention. The artisan would appreciate that the promotor and signal sequence,  
15 independent from the other, could be either the endogenous promotor or signal sequence of a polypeptide of the present invention, or alternatively, could be a heterologous signal sequence and promotor.

The specific methods described herein for controlling protein secretion levels through controlled ER aggregation are not meant to be limiting and would be  
20 generally applicable to any of the polynucleotides and polypeptides of the present invention, including variants, homologues, orthologs, and fragments therein.

**Example 21 - Alteration of Protein Glycosylation Sites to Enhance Characteristics of Polypeptides of the Invention.**

25 Many eukaryotic cell surface and proteins are post-translationally processed to incorporate N-linked and O-linked carbohydrates (Kornfeld and Kornfeld (1985) Annu. Rev. Biochem. 54:631-64; Rademacher et al., (1988) Annu. Rev. Biochem. 57:785-838). Protein glycosylation is thought to serve a variety of functions including: augmentation of protein folding, inhibition of protein aggregation,  
30 regulation of intracellular trafficking to organelles, increasing resistance to proteolysis, modulation of protein antigenicity, and mediation of intercellular adhesion (Fieldler and Simons (1995) Cell, 81:309-312; Helenius (1994) Mol. Biol. Of the Cell 5:253-265; Olden et al., (1978) Cell, 13:461-473; Caton et al., (1982) Cell, 37:417-427; Alexander and Elder (1984), Science, 226:1328-1330; and Flack et al.,  
35 (1994), J. Biol. Chem., 269:14015-14020). In higher organisms, the nature and extent of glycosylation can markedly affect the circulating half-life and bio-availability of

5 proteins by mechanisms involving receptor mediated uptake and clearance (Ashwell and Morrell, (1974), *Adv. Enzymol.*, 41:99-128; Ashwell and Harford (1982), *Ann. Rev. Biochem.*, 51:531-54). Receptor systems have been identified that are thought to play a major role in the clearance of serum proteins through recognition of various carbohydrate structures on the glycoproteins (Stockert (1995), *Physiol. Rev.*, 75:591-  
10 609; Kery et al., (1992), *Arch. Biochem. Biophys.*, 298:49-55). Thus, production strategies resulting in incomplete attachment of terminal sialic acid residues might provide a means of shortening the bioavailability and half-life of glycoproteins. Conversely, expression strategies resulting in saturation of terminal sialic acid attachment sites might lengthen protein bioavailability and half-life.

15 In the development of recombinant glycoproteins for use as pharmaceutical products, for example, it has been speculated that the pharmacodynamics of recombinant proteins can be modulated by the addition or deletion of glycosylation sites from a glycoproteins primary structure (Berman and Lasky (1985a) *Trends in Biotechnol.*, 3:51-53). However, studies have reported that the deletion of N-linked 20 glycosylation sites often impairs intracellular transport and results in the intracellular accumulation of glycosylation site variants (Machamer and Rose (1988), *J. Biol. Chem.*, 263:5955-5960; Gallagher et al., (1992), *J. Virology.*, 66:7136-7145; Collier et al., (1993), *Biochem.*, 32:7818-7823; Claffey et al., (1995) *Biochemica et Biophysica Acta*, 1246:1-9; Dube et al., (1988), *J. Biol. Chem.*, 263:17516-17521).  
25 While glycosylation site variants of proteins can be expressed intracellularly, it has proved difficult to recover useful quantities from growth conditioned cell culture medium.

Moreover, it is unclear to what extent a glycosylation site in one species will be recognized by another species glycosylation machinery. Due to the importance of 30 glycosylation in protein metabolism, particularly the secretion and/or expression of the protein, whether a glycosylation signal is recognized may profoundly determine a protein's ability to be expressed, either endogenously or recombinantly, in another organism (i.e., expressing a human protein in *E.coli*, yeast, or viral organisms; or an *E.coli*, yeast, or viral protein in human, etc.). Thus, it may be desirable to add, delete, 35 or modify a glycosylation site, and possibly add a glycosylation site of one species to a protein of another species to improve the protein's functional; bioprocess

5 purification, and/or structural characteristics (e.g., a polypeptide of the present invention).

A number of methods may be employed to identify the location of glycosylation sites within a protein. One preferred method is to run the translated protein sequence through the PROSITE computer program (Swiss Institute of 10 Bioinformatics). Once identified, the sites could be systematically deleted, or impaired, at the level of the DNA using mutagenesis methodology known in the art and available to the skilled artisan, preferably using PCR-directed mutagenesis (See Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982)). Similarly, glycosylation sites could be added, or modified at the 15 level of the DNA using similar methods, preferably PCR methods (See, Maniatis, *supra*). The results of modifying the glycosylation sites for a particular protein (e.g., solubility, secretion potential, activity, aggregation, proteolytic resistance, etc.) could then be analyzed using methods known in the art.

20 **Example 22 - Method of Enhancing the Biological Activity/Functional Characteristics of Invention through Molecular Evolution.**

Although many of the most biologically active proteins known are highly effective for their specified function in an organism, they often possess characteristics that make them undesirable for transgenic, therapeutic, and/or industrial applications. 25 Among these traits, a short physiological half-life is the most prominent problem, and is present either at the level of the protein, or the level of the protein's mRNA. The ability to extend the half-life, for example, would be particularly important for a protein's use in gene therapy, transgenic animal production, the bioprocess production and purification of the protein, and use of the protein as a chemical modulator among 30 others. Therefore, there is a need to identify novel variants of isolated proteins possessing characteristics which enhance their application as a therapeutic for treating diseases of animal origin, in addition to the protein's applicability to common industrial and pharmaceutical applications.

Thus, one aspect of the present invention relates to the ability to enhance 35 specific characteristics of invention through directed molecular evolution. Such an enhancement may, in a non-limiting example, benefit the invention's utility as an

5 essential component in a kit, the inventions physical attributes such as its solubility, structure, or codon optimization, the inventions specific biological activity, including any associated enzymatic activity, the proteins enzyme kinetics, the proteins Ki, Kcat, Km, Vmax, Kd, protein-protein activity, protein-DNA binding activity, antagonist/inhibitory activity (including direct or indirect interaction), agonist activity  
10 (including direct or indirect interaction), the proteins antigenicity (e.g., where it would be desirable to either increase or decrease the antigenic potential of the protein), the immunogenicity of the protein, the ability of the protein to form dimers, trimers, or multimers with either itself or other proteins, the antigenic efficacy of the invention, including its subsequent use a preventative treatment for disease or disease states, or  
15 as an effector for targeting diseased genes. Moreover, the ability to enhance specific characteristics of a protein may also be applicable to changing the characterized activity of an enzyme to an activity completely unrelated to its initially characterized activity. Other desirable enhancements of the invention would be specific to each individual protein, and would thus be well known in the art and contemplated by the  
20 present invention.

For example, an engineered glycine receptor may be constitutively active upon binding of its cognate ligand. Alternatively, an engineered glycine receptor may be constitutively active in the absence of glycine binding. In yet another example, an engineered glycine receptor may be capable of being activated with less than all of the  
25 regulatory factors and/or conditions typically required for glycine receptor activation (e.g., glycine binding, Cl<sup>-</sup> anion permeability, phosphorylation, conformational changes, etc.). In yet another example, an engineered glycine receptor may have altered anion Cl<sup>-</sup> permeability, and/or sensitivity to glycine receptor antagonists, such as strychnine. In yet another example, an engineered glycine  
30 receptor may have altered selectivity for its modulatory glycine receptor beta subunit, or cofactors. Such glycine receptors would be useful in screens to identify glycine receptor modulators, among other uses described herein.

Directed evolution is comprised of several steps. The first step is to establish a library of variants for the gene or protein of interest. The most important step is to  
35 then select for those variants that entail the activity you wish to identify. The design of the screen is essential since your screen should be selective enough to eliminate

5 non-useful variants, but not so stringent as to eliminate all variants. The last step is then to repeat the above steps using the best variant from the previous screen. Each successive cycle, can then be tailored as necessary, such as increasing the stringency of the screen, for example.

Over the years, there have been a number of methods developed to introduce  
10 mutations into macromolecules. Some of these methods include, random mutagenesis, “error-prone” PCR, chemical mutagenesis, site-directed mutagenesis, and other methods well known in the art (for a comprehensive listing of current mutagenesis methods, see Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982)). Typically, such methods have been used, for  
15 example, as tools for identifying the core functional region(s) of a protein or the function of specific domains of a protein (if a multi-domain protein). However, such methods have more recently been applied to the identification of macromolecule variants with specific or enhanced characteristics.

Random mutagenesis has been the most widely recognized method to date.  
20 Typically, this has been carried out either through the use of “error-prone” PCR (as described in Moore, J., et al, Nature Biotechnology 14:458, (1996), or through the application of randomized synthetic oligonucleotides corresponding to specific regions of interest (as described by Derbyshire, K.M. et al, Gene, 46:145-152, (1986), and Hill, DE, et al, Methods Enzymol., 55:559-568, (1987). Both approaches have  
25 limits to the level of mutagenesis that can be obtained. However, either approach enables the investigator to effectively control the rate of mutagenesis. This is particularly important considering the fact that mutations beneficial to the activity of the enzyme are fairly rare. In fact, using too high a level of mutagenesis may counter or inhibit the desired benefit of a useful mutation.

30 While both of the aforementioned methods are effective for creating randomized pools of macromolecule variants, a third method, termed “DNA Shuffling”, or “sexual PCR” (WPC, Stemmer, PNAS, 91:10747, (1994)) has recently been elucidated. DNA shuffling has also been referred to as “directed molecular evolution”, “exon-shuffling”, “directed enzyme evolution”, “in vitro evolution”, and  
35 “artificial evolution”. Such reference terms are known in the art and are encompassed by the invention. This new, preferred, method apparently overcomes the limitations of

5 the previous methods in that it not only propagates positive traits, but simultaneously eliminates negative traits in the resulting progeny.

DNA shuffling accomplishes this task by combining the principal of in vitro recombination, along with the method of "error-prone" PCR. In effect, you begin with a randomly digested pool of small fragments of your gene, created by Dnase I 10 digestion, and then introduce said random fragments into an "error-prone" PCR assembly reaction. During the PCR reaction, the randomly sized DNA fragments not only hybridize to their cognate strand, but also may hybridize to other DNA fragments corresponding to different regions of the polynucleotide of interest – regions not typically accessible via hybridization of the entire polynucleotide. Moreover, since the 15 PCR assembly reaction utilizes "error-prone" PCR reaction conditions, random mutations are introduced during the DNA synthesis step of the PCR reaction for all of the fragments -further diversifying the potential hybridization sites during the annealing step of the reaction.

A variety of reaction conditions could be utilized to carry-out the DNA 20 shuffling reaction. However, specific reaction conditions for DNA shuffling are provided, for example, in PNAS, 91:10747, (1994). Briefly:

Prepare the DNA substrate to be subjected to the DNA shuffling reaction. Preparation may be in the form of simply purifying the DNA from contaminating 25 cellular material, chemicals, buffers, oligonucleotide primers, deoxynucleotides, RNAs, etc., and may entail the use of DNA purification kits as those provided by Qiagen, Inc., or by the Promega, Corp., for example.

Once the DNA substrate has been purified, it would be subjected to Dnase I digestion. About 2-4ug of the DNA substrate(s) would be digested with .0015 units of Dnase I (Sigma) per ul in 100ul of 50mM Tris-HCL, pH 7.4/1mM MgCl<sub>2</sub> for 10-20 30 min. at room temperature. The resulting fragments of 10-50bp could then be purified by running them through a 2% low-melting point agarose gel by electrophoresis onto DE81 ion-exchange paper (Whatmann) or could be purified using Microcon concentrators (Amicon) of the appropriate molecular weight cutoff, or could use oligonucleotide purification columns (Qiagen), in addition to other methods known in 35 the art. If using DE81 ion-exchange paper, the 10-50bp fragments could be eluted from said paper using 1M NaCl, followed by ethanol precipitation.

5        The resulting purified fragments would then be subjected to a PCR assembly reaction by re-suspension in a PCR mixture containing: 2mM of each dNTP, 2.2mM MgCl<sub>2</sub>, 50 mM KCl, 10mM Tris•HCL, pH 9.0, and 0.1% Triton X-100, at a final fragment concentration of 10-30ng/ul. No primers are added at this point. *Taq* DNA polymerase (Promega) would be used at 2.5 units per 100ul of reaction mixture. A  
10      PCR program of 94 C for 60s; 94 C for 30s, 50-55 C for 30s, and 72 C for 30s using 30-45 cycles, followed by 72 C for 5min using an MJ Research (Cambridge, MA) PTC-150 thermocycler. After the assembly reaction is completed, a 1:40 dilution of the resulting primerless product would then be introduced into a PCR mixture (using the same buffer mixture used for the assembly reaction) containing 0.8um of each  
15      primer and subjecting this mixture to 15 cycles of PCR (using 94 C for 30s, 50 C for 30s, and 72 C for 30s). The referred primers would be primers corresponding to the nucleic acid sequences of the polynucleotide(s) utilized in the shuffling reaction. Said primers could consist of modified nucleic acid base pairs using methods known in the art and referred to else where herein, or could contain additional sequences (i.e., for  
20      adding restriction sites, mutating specific base-pairs, etc.).

      The resulting shuffled, assembled, and amplified product can be purified using methods well known in the art (e.g., Qiagen PCR purification kits) and then subsequently cloned using appropriate restriction enzymes.

      Although a number of variations of DNA shuffling have been published to date, such variations would be obvious to the skilled artisan and are encompassed by the invention. The DNA shuffling method can also be tailored to the desired level of mutagenesis using the methods described by Zhao, et al. (Nucl Acid Res., 25(6):1307-1308, (1997).

      As described above, once the randomized pool has been created, it can then be subjected to a specific screen to identify the variant possessing the desired characteristic(s). Once the variant has been identified, DNA corresponding to the variant could then be used as the DNA substrate for initiating another round of DNA shuffling. This cycle of shuffling, selecting the optimized variant of interest, and then re-shuffling, can be repeated until the ultimate variant is obtained. Examples of model screens applied to identify variants created using DNA shuffling technology may be found in the following publications: J. C., Moore, et al., J. Mol. Biol., 272:336-347,

5 (1997), F.R., Cross, et al., Mol. Cell. Biol., 18:2923-2931, (1998), and A. Crameri., et al., Nat. Biotech., 15:436-438, (1997).

DNA shuffling has several advantages. First, it makes use of beneficial mutations. When combined with screening, DNA shuffling allows the discovery of the best mutational combinations and does not assume that the best combination 10 contains all the mutations in a population. Secondly, recombination occurs simultaneously with point mutagenesis. An effect of forcing DNA polymerase to synthesize full-length genes from the small fragment DNA pool is a background mutagenesis rate. In combination with a stringent selection method, enzymatic activity has been evolved up to 16000 fold increase over the wild-type form of the 15 enzyme. In essence, the background mutagenesis yielded the genetic variability on which recombination acted to enhance the activity.

A third feature of recombination is that it can be used to remove deleterious mutations. As discussed above, during the process of the randomization, for every one beneficial mutation, there may be at least one or more neutral or inhibitory mutations. 20 Such mutations can be removed by including in the assembly reaction an excess of the wild-type random-size fragments, in addition to the random-size fragments of the selected mutant from the previous selection. During the next selection, some of the most active variants of the polynucleotide/polypeptide/enzyme, should have lost the inhibitory mutations.

25 Finally, recombination enables parallel processing. This represents a significant advantage since there are likely multiple characteristics that would make a protein more desirable (e.g. solubility, activity, etc.). Since it is increasingly difficult to screen for more than one desirable trait at a time, other methods of molecular evolution tend to be inhibitory. However, using recombination, it would be possible to 30 combine the randomized fragments of the best representative variants for the various traits, and then select for multiple properties at once.

DNA shuffling can also be applied to the polynucleotides and polypeptides of the present invention to decrease their immunogenicity in a specified host. For example, a particular variant of the present invention may be created and isolated 35 using DNA shuffling technology. Such a variant may have all of the desired characteristics, though may be highly immunogenic in a host due to its novel intrinsic

5 structure. Specifically, the desired characteristic may cause the polypeptide to have a non-native structure which could no longer be recognized as a "self" molecule, but rather as a "foreign", and thus activate a host immune response directed against the novel variant. Such a limitation can be overcome, for example, by including a copy of the gene sequence for a xenobiotic ortholog of the native protein in with the gene  
10 sequence of the novel variant gene in one or more cycles of DNA shuffling. The molar ratio of the ortholog and novel variant DNAs could be varied accordingly. Ideally, the resulting hybrid variant identified would contain at least some of the coding sequence which enabled the xenobiotic protein to evade the host immune system, and additionally, the coding sequence of the original novel variant that  
15 provided the desired characteristics.

Likewise, the invention encompasses the application of DNA shuffling technology to the evolution of polynucleotides and polypeptides of the invention, wherein one or more cycles of DNA shuffling include, in addition to the gene template DNA, oligonucleotides coding for known allelic sequences, optimized codon  
20 sequences, known variant sequences, known polynucleotide polymorphism sequences, known ortholog sequences, known homologue sequences, additional homologous sequences, additional non-homologous sequences, sequences from another species, and any number and combination of the above.

In addition to the described methods above, there are a number of related  
25 methods that may also be applicable, or desirable in certain cases. Representative among these are the methods discussed in PCT applications WO 98/31700, and WO 98/32845, which are hereby incorporated by reference. Furthermore, related methods can also be applied to the polynucleotide sequences of the present invention in order to evolve invention for creating ideal variants for use in gene therapy, protein  
30 engineering, evolution of whole cells containing the variant, or in the evolution of entire enzyme pathways containing polynucleotides of the invention as described in PCT applications WO 98/13485, WO 98/13487, WO 98/27230, WO 98/31837, and Crameri, A., et al., Nat. Biotech., 15:436-438, (1997), respectively.

Additional methods of applying "DNA Shuffling" technology to the  
35 polynucleotides and polypeptides of the present invention, including their proposed applications, may be found in US Patent No. 5,605,793; PCT Application No. WO

5 95/22625; PCT Application No. WO 97/20078; PCT Application No. WO 97/35966; and PCT Application No. WO 98/42832; PCT Application No. WO 00/09727 specifically provides methods for applying DNA shuffling to the identification of herbicide selective crops which could be applied to the polynucleotides and polypeptides of the present invention; additionally, PCT Application No. WO  
10 00/12680 provides methods and compositions for generating, modifying, adapting, and optimizing polynucleotide sequences that confer detectable phenotypic properties on plant species; each of the above are hereby incorporated in their entirety herein for all purposes.

15 **Example 23 – Method of Creating N- and C-terminal Deletion Mutants Corresponding to the HGPR4 Polypeptide of the Present Invention.**

As described elsewhere herein, the present invention encompasses the creation of N- and C-terminal deletion mutants, in addition to any combination of N- and C-terminal deletions thereof, corresponding to the HGPR4 or HGRAsv polypeptides of 20 the present invention. A number of methods are available to one skilled in the art for creating such mutants. Such methods may include a combination of PCR amplification and gene cloning methodology. Although one of skill in the art of molecular biology, through the use of the teachings provided or referenced herein, and/or otherwise known in the art as standard methods, could readily create each 25 deletion mutant of the present invention, exemplary methods are described below.

Briefly, using the isolated cDNA clone encoding the full-length HGPR4 or HGRAsv polypeptide sequence (as described in Example 11, for example), appropriate primers of about 15-25 nucleotides derived from the desired 5' and 3' positions of SEQ ID NO:1 or SEQ ID NO:3 may be designed to PCR amplify, and 30 subsequently clone, the intended N- and/or C-terminal deletion mutant. Such primers could comprise, for example, an initiation and stop codon for the 5' and 3' primer, respectively. Such primers may also comprise restriction sites to facilitate cloning of the deletion mutant post amplification. Moreover, the primers may comprise additional sequences, such as, for example, flag-tag sequences, kozac sequences, or 35 other sequences discussed and/or referenced herein.

5 For example, in the case of the E191 to D431 HGRAsv N-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'-GCAGCA <u>GCGGCCGC</u> GAGAGCTCATCCATACTCTGCAGCC -3' (SEQ ID NO:78)  <i>NotI</i>
3' Primer	5'- GCAGCA <u>GTCGAC</u> GTCCACGTAGAGTTCCCGCGTGG -3' (SEQ ID NO:79)  <i>SalI</i>

10

For example, in the case of the M1 to R358 HGRAsv C-terminal deletion mutant, the following primers could be used to amplify a cDNA fragment corresponding to this deletion mutant:

5' Primer	5'- GCAGCA <u>GCGGCCGC</u> ATGACAACTCTGTTCCCTGCAACCC -3' (SEQ ID NO:80)  <i>NotI</i>
3' Primer	5'- GCAGCA <u>GTCGAC</u> ACGAGAAACAAAATTATGGCAGC -3' (SEQ ID NO:81)  <i>SalI</i>

15

Representative PCR amplification conditions are provided below, although the skilled artisan would appreciate that other conditions may be required for efficient amplification. A 100 ul PCR reaction mixture may be prepared using 10ng of the template DNA (cDNA clone of HGPR4), 200 uM 4dNTPs, 1uM primers, 0.25U Taq DNA polymerase (PE), and standard Taq DNA polymerase buffer. Typical PCR cycling condition are as follows:

20-25 cycles: 45 sec, 93 degrees  
2 min, 50 degrees  
25 2 min, 72 degrees  
1 cycle: 10 min, 72 degrees

5 After the final extension step of PCR, 5U Klenow Fragment may be added and  
incubated for 15 min at 30 degrees.

Upon digestion of the fragment with the NotI and SalI restriction enzymes, the fragment could be cloned into an appropriate expression and/or cloning vector which has been similarly digested (e.g., pSport1, among others). . The skilled artisan would  
10 appreciate that other plasmids could be equally substituted, and may be desirable in certain circumstances. The digested fragment and vector are then ligated using a DNA ligase, and then used to transform competent E.coli cells using methods provided herein and/or otherwise known in the art.

The 5' primer sequence for amplifying any additional N-terminal deletion  
15 mutants may be determined by reference to the following formula:

(S+(X \* 3)) to ((S+(X \* 3))+25), wherein 'S' is equal to the nucleotide position of the initiating start codon of the HGPR4 or HGRAsv gene (SEQ ID NO:1 or SEQ ID NO:3), and 'X' is equal to the most N-terminal amino acid of the intended N-terminal deletion mutant. The first term will provide the start 5' nucleotide position  
20 of the 5' primer, while the second term will provide the end 3' nucleotide position of the 5' primer corresponding to sense strand of SEQ ID NO:1 or SEQ ID NO:3. Once the corresponding nucleotide positions of the primer are determined, the final nucleotide sequence may be created by the addition of applicable restriction site sequences to the 5' end of the sequence, for example. As referenced herein, the  
25 addition of other sequences to the 5' primer may be desired in certain circumstances (e.g., kozac sequences, etc.).

The 3' primer sequence for amplifying any additional N-terminal deletion mutants may be determined by reference to the following formula:

(S+(X \* 3)) to ((S+(X \* 3))-25), wherein 'S' is equal to the nucleotide position  
30 of the initiating start codon of the HGPR4 or HGRA4sv gene (SEQ ID NO:1 or SEQ ID NO:3), and 'X' is equal to the most C-terminal amino acid of the intended N-terminal deletion mutant. The first term will provide the start 5' nucleotide position of the 3' primer, while the second term will provide the end 3' nucleotide position of the 3' primer corresponding to the anti-sense strand of SEQ ID NO:1 or SEQ ID NO:3.  
35 Once the corresponding nucleotide positions of the primer are determined, the final nucleotide sequence may be created by the addition of applicable restriction site

5 sequences to the 5' end of the sequence, for example. As referenced herein, the addition of other sequences to the 3' primer may be desired in certain circumstances (e.g., stop codon sequences, etc.). The skilled artisan would appreciate that modifications of the above nucleotide positions may be necessary for optimizing PCR amplification.

10 The same general formulas provided above may be used in identifying the 5' and 3' primer sequences for amplifying any C-terminal deletion mutant of the present invention. Moreover, the same general formulas provided above may be used in identifying the 5' and 3' primer sequences for amplifying any combination of N-terminal and C-terminal deletion mutant of the present invention. The skilled artisan 15 would appreciate that modifications of the above nucleotide positions may be necessary for optimizing PCR amplification.

**Example 24 - Identification and Cloning of VH and VL domains Of Antibodies Directed Against the HGPR4 Polypeptide.**

20 VH and VL domains may be identified and cloned from cell lines expressing an antibody directed against a HGPR4 epitope by performing PCR with VH and VL specific primers on cDNA made from the antibody expressing cell lines. Briefly, RNA is isolated from the cell lines and used as a template for RT-PCR designed to amplify the VH and VL domains of the antibodies expressed by the EBV cell lines.

25 Cells may be lysed using the TRIzol reagent (Life Technologies, Rockville, MD) and extracted with one fifth volume of chloroform. After addition of chloroform, the solution is allowed to incubate at room temperature for 10 minutes, and then centrifuged at 14, 000 rpm for 15 minutes at 4 C in a tabletop centrifuge. The supernatant is collected and RNA is precipitated using an equal volume of 30 isopropanol. Precipitated RNA is pelleted by centrifuging at 14, 000 rpm for 15 minutes at 4 C in a tabletop centrifuge.

Following centrifugation, the supernatant is discarded and washed with 75% ethanol. Following the wash step, the RNA is centrifuged again at 800 rpm for 5 minutes at 4 C. The supernatant is discarded and the pellet allowed to air dry. RNA is 35 then dissolved in DEPC water and heated to 60 C for 10 minutes. Quantities of RNA can be determined using optical density measurements. cDNA may be synthesized, according to methods well-known in the art and/or described herein, from 1. 5-2. 5

5 micrograms of RNA using reverse transcriptase and random hexamer primers. cDNA is then used as a template for PCR amplification of VH and VL domains.

Primers used to amplify VH and VL genes are shown below. Typically a PCR reaction makes use of a single 5' primer and a single 3' primer. Sometimes, when the amount of available RNA template is limiting, or for greater efficiency, groups of 5' and/or 3' primers may be used. For example, sometimes all five VH-5' primers and all JH3' primers are used in a single PCR reaction. The PCR reaction is carried out in a 50 microliter volume containing 1X PCR buffer, 2mM of each dNTP, 0.7 units of High Fidelity Taq polymerase, 5' primer mix, 3' primer mix and 7.5 microliters of cDNA. The 5' and 3' primer mix of both VH and VL can be made by pooling together 22 pmole and 28 pmole, respectively, of each of the individual primers. PCR conditions are : 96 C for 5 minutes ; followed by 25 cycles of 94 C for 1 minute, 50 C for 1 minute, and 72 C for 1 minute ; followed by an extension cycle of 72 C for 10 minutes. After the reaction has been completed, sample tubes may be stored at 4 C.

20 *Primer Sequences Used to Amplify VH domains.*

Primer name	Primer Sequence	SEQ ID NO:
Hu VH1 - 5'	CAGGTGCAGCTGGTGCAGTCTGG	38
Hu VH2 - 5'	CAGGTCAACTTAAGGGAGTCTGG	39
Hu VH3 - 5'	GAGGTGCAGCTGGTGGAGTCTGG	40
Hu VH4 - 5'	CAGGTGCAGCTGCAGGAGTCGGG	41
Hu VH5 - 5'	GAGGTGCAGCTGTTGCAGTCTGC	42
Hu VH6 - 5'	CAGGTACAGCTGCAGCAGTCAGG	43
Hu JH1 - 5'	TGAGGAGACGGTGACCAGGGTGC	44
Hu JH3 - 5'	TGAAGAGACGGTGACCATTGTCCC	45
Hu JH4 - 5'	TGAGGAGACGGTGACCAGGGTTCC	46
Hu JH6 - 5'	TGAGGAGACGGTGACCGTGGTCCC	47

*Primer Sequences Used to Amplify VL domains*

Primer name	Primer Sequence	SEQ ID NO:
Hu Vkappal - 5'	GACATCCAGATGACCCAGTCTCC	48

Primer name	Primer Sequence	SEQ ID NO:
Hu Vkappa2a - 5'	GATGTTGTGATGACTCAGTCTCC	49
Hu Vkappa2b - 5'	GATATTGTGATGACTCAGTCTCC	50
Hu Vkappa3 - 5'	GAAATTGTGTTGACGCAGTCTCC	51
Hu Vkappa4 - 5'	GACATCGTGATGACCCAGTCTCC	52
Hu Vkappa5 - 5'	GAAACGACACTCACGCAGTCTCC	53
Hu Vkappa6 - 5'	GAAATTGTGCTGACTCAGTCTCC	54
Hu Vlambdal - 5'	CAGTCTGTGTTGACGCAGCCGCC	55
Hu Vlambda2 - 5'	CAGTCTGCCCTGACTCAGCCTGC	56
Hu Vlambda3 - 5'	TCCTATGTGCTGACTCAGCCACC	57
Hu Vlambda3b - 5'	TCTTCTGAGCTGACTCAGGACCC	58
Hu Vlambda4 - 5'	CACGTTATACTGACTCAACCGCC	59
Hu Vlambda5 - 5'	CAGGCTGTGCTCACTCAGCCGTC	60
Hu Vlambda6 - 5'	AATTTTATGCTGACTCAGCCCCA	61
Hu Jkappa1 - 3'	ACGTTTGATTCACCTTGGTCCC	62
Hu Jkappa2 - 3'	ACGTTTGATCTCCAGCTTGGTCCC	63
Hu Jkappa3 - 3'	ACGTTTGATATCCACTTGGTCCC	64
Hu Jkappa4 - 3'	ACGTTTGATCTCCACCTTGGTCCC	65
Hu Jkappa5 - 3'	ACGTTTAATCTCCAGTCGTGTCCC	66
Hu Vlambdal - 3'	CAGTCTGTGTTGACGCAGCCGCC	67
Hu Vlambda2 - 3'	CAGTCTGCCCTGACTCAGCCTGC	68
Hu Vlambda3 - 3'	TCCTATGTGCTGACTCAGCCACC	69
Hu Vlambda3b - 3'	TCTTCTGAGCTGACTCAGGACCC	70
Hu Vlambda4 - 3'	CACGTTATACTGACTCAACCGCC	71
Hu Vlambda5 - 3'	CAGGCTGTGCTCACTCAGCCGTC	72
Hu Vlambda6 - 3'	AATTTTATGCTGACTCAGCCCCA	73

5

PCR samples are then electrophoresed on a 1.3% agarose gel. DNA bands of the expected sizes (-506 base pairs for VH domains, and 344 base pairs for VL domains) can be cut out of the gel and purified using methods well known in the art and/or described herein.

10 Purified PCR products can be ligated into a PCR cloning vector (TA vector from Invitrogen Inc., Carlsbad, CA). Individual cloned PCR products can be isolated

5 after transfection of *E. coli* and blue/white color selection. Cloned PCR products may then be sequenced using methods commonly known in the art and/or described herein.

The PCR bands containing the VH domain and the VL domains can also be used to create full-length Ig expression vectors. VH and VL domains can be cloned into vectors containing the nucleotide sequences of a heavy (e. g., human IgG1 or 10 human IgG4) or light chain (human kappa or human lambda) constant regions such that a complete heavy or light chain molecule could be expressed from these vectors when transfected into an appropriate host cell. Further, when cloned heavy and light chains are both expressed in one cell line (from either one or two vectors), they can assemble into a complete functional antibody molecule that is secreted into the cell 15 culture medium. Methods using polynucleotides encoding VH and VL antibody domain to generate expression vectors that encode complete antibody molecules are well known within the art.

20 **Example 25 - Method of Determining Alterations in a Gene Corresponding to a Polynucleotide**

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is 25 then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:1. Suggested PCR conditions consist of 35 cycles at 95 degrees C for 30 seconds; 60-120 seconds at 52-58 degrees C; and 60-120 seconds at 70 degrees C, using buffer solutions described in Sidransky et al., *Science* 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 30 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton et al., 35 *Nucleic Acids Research*, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

5        Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 11 are nick-translated with digoxigenin-deoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is  
10      carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, 15      Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the 20      genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

**Example 26 - Method of Detecting Abnormal Levels of a Polypeptide in a  
25      Biological Sample**

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their 30      particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described elsewhere 35      herein. The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

5 The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

10 Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

15 Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

20

### **Example 27 - Formulation**

The invention also provides methods of treatment and/or prevention diseases, disorders, and/or conditions (such as, for example, any one or more of the diseases or disorders disclosed herein) by administration to a subject of an effective amount of a Therapeutic. By therapeutic is meant a polynucleotides or polypeptides of the invention (including fragments and variants), agonists or antagonists thereof, and/or antibodies thereto, in combination with a pharmaceutically acceptable carrier type (e.g., a sterile carrier).

30 The Therapeutic will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the Therapeutic alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

35 As a general proposition, the total pharmaceutically effective amount of the Therapeutic administered parenterally per dose will be in the range of about

5 1 ug/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the Therapeutic is typically administered at a dose rate of about 1 ug/kg/hour to about 50 ug/kg/hour, either by 1-4 injections per  
10 day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Therapeutics can be administered orally, rectally, parenterally, intracisternally, 15 intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, 20 intrasternal, subcutaneous and intraarticular injection and infusion.

In yet an additional embodiment, the Therapeutics of the invention are delivered orally using the drug delivery technology described in U.S. Patent 6,258,789, which is hereby incorporated by reference herein.

Therapeutics of the invention are also suitably administered by sustained- 25 release systems. Suitable examples of sustained-release Therapeutics are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation 30 auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention may also be suitably administered by sustained- 35 release systems. Suitable examples of sustained-release Therapeutics include suitable polymeric materials (such as, for example, semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules), suitable hydrophobic materials

5 (for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (Langer et al., 10 J. Biomed. Mater. Res. 15:167-277 (1981), and Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., Id.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988).

Sustained-release Therapeutics also include liposomally entrapped Therapeutics of the invention (see, generally, Langer, Science 249:1527-1533 (1990); 15 Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 317 -327 and 353-365 (1989)). Liposomes containing the Therapeutic are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. (USA) 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci.(USA) 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 20 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal Therapeutic.

25 In yet an additional embodiment, the Therapeutics of the invention are delivered by way of a pump (see Langer, *supra*; Sefton, CRC Crit. Ref. Biomed. Eng. 14:201 (1987); Buchwald et al., Surgery 88:507 (1980); Saudek et al., N. Engl. J. Med. 321:574 (1989)).

Other controlled release systems are discussed in the review by Langer 30 (Science 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Therapeutic is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. 35 For example, the formulation preferably does not include oxidizing agents and other

5 compounds that are known to be deleterious to the Therapeutic.

Generally, the formulations are prepared by contacting the Therapeutic uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood 10 of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances 15 that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as 20 polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

25 The Therapeutic will typically be formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any pharmaceutical used for therapeutic administration can be sterile. Sterility 30 is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutics generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Therapeutics ordinarily will be stored in unit or multi-dose containers, for 35 example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml

5 vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Therapeutic solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized Therapeutic using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the Therapeutics of the 10 invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the Therapeutics may be employed in conjunction with other therapeutic compounds.

15 The Therapeutics of the invention may be administered alone or in combination with adjuvants. Adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG, and MPL. In a specific embodiment, Therapeutics of the invention are administered in 20 combination with alum. In another specific embodiment, Therapeutics of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, Monophosphoryl lipid immunomodulator, AdjuVax 100a, QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Virosomal adjuvant technology. Vaccines that may be 25 administered with the Therapeutics of the invention include, but are not limited to, vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diphtheria, hepatitis A, hepatitis B, haemophilus influenzae B, whooping cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis.

30 Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the 35 same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

5        The Therapeutics of the invention may be administered alone or in combination with other therapeutic agents. Therapeutic agents that may be administered in combination with the Therapeutics of the invention, include but not limited to, other members of the TNF family, chemotherapeutic agents, antibiotics, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic  
10      agents, cytokines and/or growth factors. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through  
15      separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

      In one embodiment, the Therapeutics of the invention are administered in combination with members of the TNF family. TNF, TNF-related or TNF-like  
20      molecules that may be administered with the Therapeutics of the invention include, but are not limited to, soluble forms of TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No.  
25      WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), TR6 (International Publication No. WO 98/30694), OPG, and neutrokine-alpha (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-IBB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904),  
30      DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms  
35      CD154, CD70, and CD153.

      In certain embodiments, Therapeutics of the invention are administered in

5 combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors. Nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, RETROVIR( zidovudine/AZT), VIDEX( didanosine/ddI), HIVID( zalcitabine/ddC), ZERIT( stavudine/d4T), EPIVIR( lamivudine/3TC), and COMBIVIR( zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, VIRAMUNE( nevirapine), DESCRIPTOR( delavirdine), and SUSTIVA( efavirenz). Protease inhibitors that may be administered in combination 10 with the Therapeutics of the invention, include, but are not limited to, CRIXIVAN( indinavir), NORVIR( ritonavir), INVIRASE( saquinavir), and VIRACEPT( nelfinavir). In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors may be used in any combination with Therapeutics of the 15 invention to treat AIDS and/or to prevent or treat HIV infection.

20

In other embodiments, Therapeutics of the invention may be administered in combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE(, DAPSONE(, 25 PENTAMIDINE(, ATOVAQUONE(, ISONIAZID(, RIFAMPIN(, PYRAZINAMIDE(, ETHAMBUTOL(, RIFABUTIN(, CLARITHROMYCIN(, AZITHROMYCIN(, GANCICLOVIR(, FOSCARNET(, CIDOFOVIR(, FLUCONAZOLE(, ITRACONAZOLE(, KETOCONAZOLE(, ACYCLOVIR(, FAMCICOLVIR(, PYRIMETHAMINE(, LEUCOVORIN(, NEUPOGEN(, 30 (filgrastim/G-CSF), and LEUKINE( (sargramostim/GM-CSF). In a specific embodiment, Therapeutics of the invention are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE(, DAPSONE(, PENTAMIDINE(, and/or ATOVAQUONE( to prophylactically treat or prevent an opportunistic *Pneumocystis carinii* pneumonia infection. In another specific embodiment, 35 Therapeutics of the invention are used in any combination with ISONIAZID(, RIFAMPIN(, PYRAZINAMIDE(, and/or ETHAMBUTOL( to prophylactically treat

5 or prevent an opportunistic *Mycobacterium avium* complex infection. In another specific embodiment, Therapeutics of the invention are used in any combination with RIFABUTIN(, CLARITHROMYCIN(, and/or AZITHROMYCIN( to prophylactically treat or prevent an opportunistic *Mycobacterium tuberculosis* infection. In another specific embodiment, Therapeutics of the invention are used in  
10 any combination with GANCICLOVIR(, FOSCARNET(, and/or CIDOFOVIR( to prophylactically treat or prevent an opportunistic cytomegalovirus infection. In another specific embodiment, Therapeutics of the invention are used in any combination with FLUCONAZOLE(, ITRACONAZOLE(, and/or KETOCONAZOLE( to prophylactically treat or prevent an opportunistic fungal  
15 infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ACYCLOVIR( and/or FAMCICOLVIR( to prophylactically treat or prevent an opportunistic herpes simplex virus type I and/or type II infection. In another specific embodiment, Therapeutics of the invention are used in any combination with PYRIMETHAMINE( and/or LEUCOVORIN( to prophylactically  
20 treat or prevent an opportunistic *Toxoplasma gondii* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with LEUCOVORIN( and/or NEUPOGEN( to prophylactically treat or prevent an opportunistic bacterial infection.

In a further embodiment, the Therapeutics of the invention are administered in  
25 combination with an antiviral agent. Antiviral agents that may be administered with the Therapeutics of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.

In a further embodiment, the Therapeutics of the invention are administered in combination with an antibiotic agent. Antibiotic agents that may be administered with  
30 the Therapeutics of the invention include, but are not limited to, amoxicillin, beta-lactamases, aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin, erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin, sulfonamide, tetracyclines, trimethoprim, trimethoprim-  
35 sulfamthoxazole, and vancomycin.

Conventional nonspecific immunosuppressive agents, that may be

5 administered in combination with the Therapeutics of the invention include, but are not limited to, steroids, cyclosporine, cyclosporine analogs, cyclophosphamide methylprednisolone, prednisone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive agents that act by suppressing the function of responding T cells.

In specific embodiments, Therapeutics of the invention are administered in  
10 combination with immunosuppressants. Immunosuppressants preparations that may be administered with the Therapeutics of the invention include, but are not limited to, ORTHOCLONE( (OKT3), SANDIMMUNE/NEORAL(/SANGDYA( (cyclosporin), PROGRAF( (tacrolimus), CELLCEPT( (mycophenolate), Azathioprine, glucorticosteroids, and RAPAMUNE( (sirolimus). In a specific embodiment,  
15 immunosuppressants may be used to prevent rejection of organ or bone marrow transplantation.

In an additional embodiment, Therapeutics of the invention are administered alone or in combination with one or more intravenous immune globulin preparations. Intravenous immune globulin preparations that may be administered with the  
20 Therapeutics of the invention include, but not limited to, GAMMAR(, IVEEGAM(, SANDOGLOBULIN(, GAMMAGARD S/D(, and GAMIMUNE(. In a specific embodiment, Therapeutics of the invention are administered in combination with intravenous immune globulin preparations in transplantation therapy (e.g., bone marrow transplant).

25 In an additional embodiment, the Therapeutics of the invention are administered alone or in combination with an anti-inflammatory agent. Anti-inflammatory agents that may be administered with the Therapeutics of the invention include, but are not limited to, glucocorticoids and the nonsteroidal anti-inflammatories, aminoarylcarboxylic acid derivatives, arylacetic acid derivatives,  
30 arylbutyric acid derivatives, arylcarboxylic acids, arylpropionic acid derivatives, pyrazoles, pyrazolones, salicylic acid derivatives, thiazinecarboxamides, e-acetamidocaproic acid, S-adenosylmethionine, 3-amino-4-hydroxybutyric acid, amixetidine, bendazac, benzydamine, bucolome, difenpiramide, ditazol, emorfazone, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol, paranyline, perisoxal,  
35 pifoxime, proquazone, proxazole, and tenidap.

In another embodiment, compositions of the invention are administered in

5 combination with a chemotherapeutic agent. Chemotherapeutic agents that may be administered with the Therapeutics of the invention include, but are not limited to, antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin); antiestrogens (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-FU, methotrexate, floxuridine, interferon alpha-2b, glutamic acid, plicamycin, 10 mercaptourine, and 6-thioguanine); cytotoxic agents (e.g., carmustine, BCNU, lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol 15 diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., mephalen, chorambucil, mechlorethamine (nitrogen mustard) and thiotepa); steroids and combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dacarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

20 In a specific embodiment, Therapeutics of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or any combination of the components of CHOP. In another embodiment, Therapeutics of the invention are administered in combination with Rituximab. In a further embodiment, Therapeutics of the invention are administered with Rituximab 25 and CHOP, or Rituximab and any combination of the components of CHOP.

In an additional embodiment, the Therapeutics of the invention are administered in combination with cytokines. Cytokines that may be administered with the Therapeutics of the invention include, but are not limited to, IL2, IL3, IL4, IL5, IL6, IL7, IL10, IL12, IL13, IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha. In 30 another embodiment, Therapeutics of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21.

In an additional embodiment, the Therapeutics of the invention are 35 administered in combination with angiogenic proteins. Angiogenic proteins that may be administered with the Therapeutics of the invention include, but are not limited to,

5 Glioma Derived Growth Factor (GDGF), as disclosed in European Patent Number EP-399816; Platelet Derived Growth Factor-A (PDGF-A), as disclosed in European Patent Number EP-682110; Platelet Derived Growth Factor-B (PDGF-B), as disclosed in European Patent Number EP-282317; Placental Growth Factor (PIGF), as disclosed in International Publication Number WO 92/06194; Placental Growth Factor-2 (PIGF-2), as disclosed in Hauser et al., Gorwth Factors, 4:259-268 (1993);  
10 Vascular Endothelial Growth Factor (VEGF), as disclosed in International Publication Number WO 90/13649; Vascular Endothelial Growth Factor-A (VEGF-A), as disclosed in European Patent Number EP-506477; Vascular Endothelial Growth Factor-2 (VEGF-2), as disclosed in International Publication Number WO 96/39515;  
15 Vascular Endothelial Growth Factor B (VEGF-3); Vascular Endothelial Growth Factor B-186 (VEGF-B186), as disclosed in International Publication Number WO 96/26736; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/02543; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/07832;  
20 and Vascular Endothelial Growth Factor-E (VEGF-E), as disclosed in German Patent Number DE19639601. The above mentioned references are incorporated herein by reference herein.

In an additional embodiment, the Therapeutics of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the Therapeutics of the invention include, but are not limited to, LEUKINE( (SARGRAMOSTIM) and NEUPOGEN( (FILGRASTIM).

In a specific embodiment, formulations of the present invention may further comprise antagonists of P-glycoprotein (also referred to as the multiresistence protein, or PGP), including antagonists of its encoding polynucleotides (e.g., antisense oligonucleotides, ribozymes, zinc-finger proteins, etc.). P-glycoprotein is well known for decreasing the efficacy of various drug administrations due to its ability to export intracellular levels of absorbed drug to the cell exterior. While this activity has been particularly pronounced in cancer cells in response to the administration of chemotherapy regimens, a variety of other cell types and the administration of other drug classes have been noted (e.g., T-cells and anti-HIV drugs). In fact, certain

5 mutations in the PGP gene significantly reduces PGP function, making it less able to force drugs out of cells. People who have two versions of the mutated gene--one inherited from each parent--have more than four times less PGP than those with two normal versions of the gene. People may also have one normal gene and one mutated one. Certain ethnic populations have increased incidence of such PGP mutations.

10 Among individuals from Ghana, Kenya, the Sudan, as well as African Americans, frequency of the normal gene ranged from 73% to 84%. In contrast, the frequency was 34% to 59% among British whites, Portuguese, Southwest Asian, Chinese, Filipino and Saudi populations. As a result, certain ethnic populations may require increased administration of PGP antagonist in the formulation of the present invention

15 to arrive at the an efficacious dose of the therapeutic (e.g., those from African descent). Conversely, certain ethnic populations, particularly those having increased frequency of the mutated PGP (e.g., of Caucasian descent, or non-African descent) may require less pharmaceutical compositions in the formulation due to an effective increase in efficacy of such compositions as a result of the increased effective

20 absorption (e.g., less PGP activity) of said composition.

Moreover, in another specific embodiment, formulations of the present invention may further comprise antagonists of OATP2 (also referred to as the multiresistance protein, or MRP2), including antagonists of its encoding polynucleotides (e.g., antisense oligonucleotides, ribozymes, zinc-finger proteins, etc.). The invention also further comprises any additional antagonists known to inhibit proteins thought to be attributable to a multidrug resistant phenotype in proliferating cells.

In an additional embodiment, the Therapeutics of the invention are administered in combination with Fibroblast Growth Factors. Fibroblast Growth Factors that may be administered with the Therapeutics of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

In additional embodiments, the Therapeutics of the invention are administered in combination with other therapeutic or prophylactic regimens, such as, for example, radiation therapy.

**5 Example 28 - Method of Treating Decreased Levels of the Polypeptide**

The present invention relates to a method for treating an individual in need of an increased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an agonist of the invention (including polypeptides of the invention). Moreover, it will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a Therapeutic comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided herein.

**Example 29 - Method of Treating Increased Levels of the Polypeptide**

The present invention also relates to a method of treating an individual in need of a decreased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an antagonist of the invention (including polypeptides and antibodies of the invention).

In one example, antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer. For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided herein.

**5 Example 30 - Method of Treatment Using Gene Therapy-Ex Vivo**

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of

10 a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37 degree C for

15 approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

20 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

25 The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 11 using primers and having appropriate restriction sites and initiation/stop codons, if necessary. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is

30 maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

35 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the

5 gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, 10 containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no 15 selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or 20 after having been grown to confluence on cytodex 3 microcarrier beads.

**Example 31 - Gene Therapy Using Endogenous Genes Corresponding To Polynucleotides of the Invention**

Another method of gene therapy according to the present invention involves 25 operably associating the endogenous polynucleotide sequence of the invention with a promoter via homologous recombination as described, for example, in U.S. Patent NO: 5,641,670, issued June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA, 86:8932-8935 30 (1989); and Zijlstra et al., Nature, 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made which contain a promoter and targeting 35 sequences, which are homologous to the 5' non-coding sequence of endogenous polynucleotide sequence, flanking the promoter. The targeting sequence will be sufficiently near the 5' end of the polynucleotide sequence so the promoter will be

5 operably linked to the endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second 10 targeting sequence contains the same restriction site as the 3' end of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added 15 together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol precipitation.

In this Example, the polynucleotide constructs are administered as naked 20 polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, precipitating agents, etc. Such methods of delivery are known in the art.

Once the cells are transfected, homologous recombination will take place 25 which results in the promoter being operably linked to the endogenous polynucleotide sequence. This results in the expression of polynucleotide corresponding to the polynucleotide in the cell. Expression may be detected by immunological staining, or any other method known in the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is 30 placed in DMEM + 10% fetal calf serum. Exponentially growing or early stationary phase fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining cells are subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 35 5 mM KCl, 0.7 mM Na<sub>2</sub>HPO<sub>4</sub>, 6 mM dextrose). The cells are recentrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1

5 mg/ml acetylated bovine serum albumin. The final cell suspension contains approximately 3X10<sup>6</sup> cells/ml. Electroporation should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the locus corresponding to the polynucleotide of 10 the invention, plasmid pUC18 (MBI Fermentas, Amherst, NY) is digested with HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on the 3'end. Two non-coding sequences are amplified via PCR: one non-coding sequence (fragment 1) is amplified with a HindIII site at the 5' end and an XbaI site at the 3'end; the other non-coding sequence (fragment 2) is amplified with a 15 BamHI site at the 5'end and a HindIII site at the 3'end. The CMV promoter and the fragments (1 and 2) are digested with the appropriate enzymes (CMV promoter - XbaI and BamHI; fragment 1 - XbaI; fragment 2 - BamHI) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

20 Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap (Bio-Rad). The final DNA concentration is generally at least 120 µg/ml. 0.5 ml of the cell suspension (containing approximately 1.5.X10<sup>6</sup> cells) is then added to the cuvette, and the cell suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 25 960 µF and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 30 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a 10 cm dish and incubated at 37 degree C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.

35 The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts

5 now produce the protein product. The fibroblasts can then be introduced into a patient as described above.

### **Example 32 - Method of Treatment Using Gene Therapy - In Vivo**

Another aspect of the present invention is using in vivo gene therapy methods 10 to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to increase or decrease the expression of the polypeptide. The polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the polypeptide by the 15 target tissue. Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata et al., *Cardiovasc. Res.* 35(3):470-479 (1997); Chao et al., *Pharmacol. Res.* 35(6):517-522 (1997); Wolff, *Neuromuscul. Disord.* 7(5):314-318 (1997); Schwartz et al., *Gene Ther.* 3(5):405-411 (1996); Tsurumi et al., *Circulation* 20 94(12):3281-3290 (1996) (incorporated herein by reference).

The polynucleotide constructs may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). The polynucleotide constructs can be delivered in a pharmaceutically acceptable liquid or 25 aqueous carrier.

The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the present 30 invention may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) *Ann. NY Acad. Sci.* 772:126-139 and Abdallah B. et al. (1995) *Biol. Cell* 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

The polynucleotide vector constructs used in the gene therapy method are 35 preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Any strong promoter known to those skilled in

5 the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

10 The polynucleotide construct can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, 15 mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred 20 for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. In vivo muscle 25 cells are particularly competent in their ability to take up and express polynucleotides.

For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as 30 the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of 35 tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or

5 mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle in vivo is determined as follows. Suitable template DNA for production of mRNA coding for polypeptide of the present invention is prepared in accordance with a standard 10 recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on 15 the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

20 After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15 um cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in 25 muscle following injection may be determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be used to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA.

30

**Example 33 - Transgenic Animals.**

The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, e.g., 35 baboons, monkeys, and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are

5 used to express polypeptides of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (i.e., polynucleotides of the invention) into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to, pronuclear 10 microinjection (Paterson et al., *Appl. Microbiol. Biotechnol.* 40:691-698 (1994); Carver et al., *Biotechnology (NY)* 11:1263-1270 (1993); Wright et al., *Biotechnology (NY)* 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., *Proc. Natl. Acad. Sci., USA* 82:6148-6152 (1985)), blastocysts or embryos; gene targeting in embryonic 15 stem cells (Thompson et al., *Cell* 56:313-321 (1989)); electroporation of cells or embryos (Lo, 1983, *Mol Cell. Biol.* 3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, e.g., Ulmer et al., *Science* 259:1745 (1993); introducing nucleic acid constructs into embryonic pluripotent 20 stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Lavitrano et al., *Cell* 57:717-723 (1989); etc. For a review of such techniques, see Gordon, "Transgenic Animals," *Intl. Rev. Cytol.* 115:171-229 (1989), which is incorporated by reference herein in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into 25 enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence (Campell et al., *Nature* 380:64-66 (1996); Wilmut et al., *Nature* 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their 30 cells, i.e., mosaic animals or chimeric. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., *Proc. Natl. Acad. Sci. USA* 89:6232-6236 (1992)). The regulatory 35 sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it

5 is desired that the polynucleotide transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the  
10 nucleotide sequence of the endogenous gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example, the teaching of Gu et al. (Gu et al., *Science* 265:103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent  
15 to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA  
20 expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, and reverse transcriptase-PCR(RT-PCR).. Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies  
25 specific for the transgene product.

Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate  
30 lines in order to produce compound transgenics that express the transgene at higher levels because of the effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment expression and eliminate the need for screening of animals by DNA analysis; crossing of separate homozygous lines to  
35 produce compound heterozygous or homozygous lines; and breeding to place the transgene on a distinct background that is appropriate for an experimental model of

5 interest.

Transgenic animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying diseases, disorders, and/or conditions associated with aberrant expression, and in screening for compounds effective in 10 ameliorating such diseases, disorders, and/or conditions.

**Example 34 - Knock-Out Animals.**

Endogenous gene expression can also be reduced by inactivating or "knocking out" the gene and/or its promoter using targeted homologous recombination. (E.g., see 15 Smithies et al., *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson et al., *Cell* 5:313-321 (1989); each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional polynucleotide of the invention (or a completely unrelated DNA sequence) flanked by DNA 20 homologous to the endogenous polynucleotide sequence (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express polypeptides of the invention *in vivo*. In another embodiment, techniques known in the art are used to generate knockouts in cells that contain, but do not express the gene of interest. Insertion of the DNA construct, via targeted homologous recombination, results in 25 inactivation of the targeted gene. Such approaches are particularly suited in research and agricultural fields where modifications to embryonic stem cells can be used to generate animal offspring with an inactive targeted gene (e.g., see Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be routinely adapted for use in humans provided the recombinant DNA constructs are directly 30 administered or targeted to the required site *in vivo* using appropriate viral vectors that will be apparent to those of skill in the art.

In further embodiments of the invention, cells that are genetically engineered to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (e.g., knockouts) are 35 administered to a patient *in vivo*. Such cells may be obtained from the patient (i.e., animal, including human) or an MHC compatible donor and can include, but are not

5 limited to fibroblasts, bone marrow cells, blood cells (e.g., lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered in vitro using recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention,  
10 e.g., by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YACs, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve  
15 expression, and preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the patient systemically, e.g., in the circulation, or intraperitoneally.

20 Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, for example, Anderson et al. U.S. Patent No. 5,399,349; and Mulligan & Wilson, U.S. Patent No. 5,460,959 each of which is incorporated by reference herein in its entirety).

25 When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does  
30 not allow the introduced cells to be recognized by the host immune system.

35 Transgenic and “knock-out” animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying diseases, disorders, and/or conditions associated with aberrant expression, and in screening for compounds effective in ameliorating such diseases, disorders, and/or conditions.

**5 Example 35 - Production of an Antibody****a) Hybridoma Technology**

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing HGRA4 are administered to an animal to induce the production of sera 10 containing polyclonal antibodies. In a preferred method, a preparation of HGRA4 protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

Monoclonal antibodies specific for protein HGRA4 are prepared using 15 hybridoma technology. (Kohler et al., *Nature* 256:495 (1975); Kohler et al., *Eur. J. Immunol.* 6:511 (1976); Kohler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981)). In general, an animal (preferably a mouse) is immunized with HGRA4 20 polypeptide or, more preferably, with a secreted HGRA4 polypeptide-expressing cell. Such polypeptide-expressing cells are cultured in any suitable tissue culture medium, preferably in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma 25 cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (*Gastroenterology* 80:225-232 (1981)). The hybridoma 30 cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the HGRA4 polypeptide.

Alternatively, additional antibodies capable of binding to HGRA4 polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it 35 is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal,

5 preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the HGRA4 protein-specific antibody can be blocked by HGRA4. Such antibodies comprise anti-idiotypic antibodies to the HGRA4 protein-specific antibody and are used to immunize an animal to induce  
10 formation of further HGRA4 protein-specific antibodies.

For in vivo use of antibodies in humans, an antibody is "humanized". Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric and humanized antibodies are known in the art and are discussed herein.  
15 (See, for review, Morrison, *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., *Nature* 312:643 (1984); Neuberger et al., *Nature* 314:268 (1985).)

20 b) Isolation Of Antibody Fragments Directed  
Against HGRA4 From A Library Of scFvs

Naturally occurring V-genes isolated from human PBLs are constructed into a library of antibody fragments which contain reactivities against HGRA4 to which the donor may or may not have been exposed (see e.g., U.S. Patent 5,885,793  
25 incorporated herein by reference in its entirety).

Rescue of the Library. A library of scFvs is constructed from the RNA of human PBLs as described in PCT publication WO 92/01047. To rescue phage displaying antibody fragments, approximately 109 E. coli harboring the phagemid are used to inoculate 50 ml of 2xTY containing 1% glucose and 100 µg/ml of ampicillin  
30 (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to inoculate 50 ml of 2xTY-AMP-GLU, 2 x 108 TU of delta gene 3 helper (M13 delta gene III, see PCT publication WO 92/01047) are added and the culture incubated at 37°C for 45 minutes without shaking and then at 37°C for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2xTY containing 100 µg/ml ampicillin and 50 µg/ml  
35 kanamycin and grown overnight. Phage are prepared as described in PCT publication

5 WO 92/01047.

M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III particles are made by growing the helper phage in cells harboring a pUC19 derivative supplying  
10 the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at 37° C without shaking and then for a further hour at 37°C with shaking. Cells are spun down (IEC-Centra 8,400 r.p.m. for 10 min), resuspended in 300 ml 2xTY broth containing 100 µg ampicillin/ml and 25 µg kanamycin/ml (2xTY-AMP-KAN) and grown overnight, shaking at 37°C. Phage particles are purified and  
15 concentrated from the culture medium by two PEG-precipitations (Sambrook et al., 1990), resuspended in 2 ml PBS and passed through a 0.45 µm filter (Minisart NML; Sartorius) to give a final concentration of approximately 1013 transducing units/ml (ampicillin-resistant clones).

Panning of the Library. Immunotubes (Nunc) are coated overnight in PBS  
20 with 4 ml of either 100 µg/ml or 10 µg/ml of a polypeptide of the present invention. Tubes are blocked with 2% Marvel-PBS for 2 hours at 37°C and then washed 3 times in PBS. Approximately 1013 TU of phage is applied to the tube and incubated for 30 minutes at room temperature tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes are washed 10 times with PBS 0.1% Tween-20  
25 and 10 times with PBS. Phage are eluted by adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable after which the solution is immediately neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4. Phage are then used to infect 10 ml of mid-log E. coli TG1 by incubating eluted phage with bacteria for 30 minutes at 37°C. The E. coli are then plated on TYE plates containing 1% glucose and  
30 100 µg/ml ampicillin. The resulting bacterial library is then rescued with delta gene 3 helper phage as described above to prepare phage for a subsequent round of selection. This process is then repeated for a total of 4 rounds of affinity purification with tube-washing increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

35 Characterization of Binders. Eluted phage from the 3rd and 4th rounds of selection are used to infect E. coli HB 2151 and soluble scFv is produced (Marks, et

5 al., 1991) from single colonies for assay. ELISAs are performed with microtitre plates coated with either 10 pg/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones positive in ELISA are further characterized by PCR fingerprinting (see, e.g., PCT publication WO 92/01047) and then by sequencing. These ELISA positive clones may also be further characterized by techniques known  
10 in the art, such as, for example, epitope mapping, binding affinity, receptor signal transduction, ability to block or competitively inhibit antibody/antigen binding, and competitive agonistic or antagonistic activity.

#### **Example 36 - Biological Effects of Polypeptides of the Invention**

15 Astrocyte and Neuronal Assays.

Recombinant polypeptides of the invention, expressed in *Escherichia coli* and purified as described above, can be tested for activity in promoting the survival, neurite outgrowth, or phenotypic differentiation of cortical neuronal cells and for inducing the proliferation of glial fibrillary acidic protein immunopositive cells, 20 astrocytes. The selection of cortical cells for the bioassay is based on the prevalent expression of FGF-1 and FGF-2 in cortical structures and on the previously reported enhancement of cortical neuronal survival resulting from FGF-2 treatment. A thymidine incorporation assay, for example, can be used to elucidate a polypeptide of the invention's activity on these cells.

25 Moreover, previous reports describing the biological effects of FGF-2 (basic FGF) on cortical or hippocampal neurons *in vitro* have demonstrated increases in both neuron survival and neurite outgrowth (Wallicke et al., "Fibroblast growth factor promotes survival of dissociated hippocampal neurons and enhances neurite extension." Proc. Natl. Acad. Sci. USA 83:3012-3016. (1986), assay herein incorporated by reference in its entirety). However, reports from experiments done on PC-12 cells suggest that these two responses are not necessarily synonymous and may depend on not only which FGF is being tested but also on which receptor(s) are expressed on the target cells. Using the primary cortical neuronal culture paradigm, the ability of a polypeptide of the invention to induce neurite outgrowth can be 30 compared to the response achieved with FGF-2 using, for example, a thymidine incorporation assay.

Fibroblast and endothelial cell assays.

Human lung fibroblasts are obtained from Clonetics (San Diego, CA) and maintained in growth media from Clonetics. Dermal microvascular endothelial cells are obtained from Cell Applications (San Diego, CA). For proliferation assays, the 10 human lung fibroblasts and dermal microvascular endothelial cells can be cultured at 5,000 cells/well in a 96-well plate for one day in growth medium. The cells are then incubated for one day in 0.1% BSA basal medium. After replacing the medium with fresh 0.1% BSA medium, the cells are incubated with the test proteins for 3 days. Alamar Blue (Alamar Biosciences, Sacramento, CA) is added to each well to a final 15 concentration of 10%. The cells are incubated for 4 hr. Cell viability is measured by reading in a CytoFluor fluorescence reader. For the PGE2 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or polypeptides of the invention with or without IL-1( for 24 hours. The supernatants are 20 collected and assayed for PGE2 by EIA kit (Cayman, Ann Arbor, MI). For the IL-6 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or with or without polypeptides of the invention IL-1( for 24 hours. The supernatants are collected and assayed for IL-6 by ELISA kit (Endogen, 25 Cambridge, MA).

Human lung fibroblasts are cultured with FGF-2 or polypeptides of the invention for 3 days in basal medium before the addition of Alamar Blue to assess effects on growth of the fibroblasts. FGF-2 should show a stimulation at 10 - 2500 ng/ml which can be used to compare stimulation with polypeptides of the invention.

Parkinson Models.

The loss of motor function in Parkinson's disease is attributed to a deficiency of striatal dopamine resulting from the degeneration of the nigrostriatal dopaminergic projection neurons. An animal model for Parkinson's that has been extensively 35 characterized involves the systemic administration of 1-methyl-4 phenyl 1,2,3,6-tetrahydropyridine (MPTP). In the CNS, MPTP is taken-up by astrocytes and

5 catabolized by monoamine oxidase B to 1-methyl-4-phenyl pyridine (MPP<sup>+</sup>) and released. Subsequently, MPP<sup>+</sup> is actively accumulated in dopaminergic neurons by the high-affinity reuptake transporter for dopamine. MPP<sup>+</sup> is then concentrated in mitochondria by the electrochemical gradient and selectively inhibits nicotidamide adenine disphosphate: ubiquinone oxidoreductionase (complex I), thereby interfering  
10 with electron transport and eventually generating oxygen radicals.

It has been demonstrated in tissue culture paradigms that FGF-2 (basic FGF) has trophic activity towards nigral dopaminergic neurons (Ferrari et al., Dev. Biol. 1989). Recently, Dr. Unsicker's group has demonstrated that administering FGF-2 in gel foam implants in the striatum results in the near complete protection of nigral  
15 dopaminergic neurons from the toxicity associated with MPTP exposure (Otto and Unsicker, J. Neuroscience, 1990).

Based on the data with FGF-2, polypeptides of the invention can be evaluated to determine whether it has an action similar to that of FGF-2 in enhancing dopaminergic neuronal survival in vitro and it can also be tested in vivo for protection  
20 of dopaminergic neurons in the striatum from the damage associated with MPTP treatment. The potential effect of a polypeptide of the invention is first examined in vitro in a dopaminergic neuronal cell culture paradigm. The cultures are prepared by dissecting the midbrain floor plate from gestation day 14 Wistar rat embryos. The tissue is dissociated with trypsin and seeded at a density of 200,000 cells/cm<sup>2</sup> on  
25 polyorthinine-laminin coated glass coverslips. The cells are maintained in Dulbecco's Modified Eagle's medium and F12 medium containing hormonal supplements (N1). The cultures are fixed with paraformaldehyde after 8 days in vitro and are processed for tyrosine hydroxylase, a specific marker for dopaminergic neurons, immunohistochemical staining. Dissociated cell cultures are prepared from embryonic  
30 rats. The culture medium is changed every third day and the factors are also added at that time.

Since the dopaminergic neurons are isolated from animals at gestation day 14, a developmental time which is past the stage when the dopaminergic precursor cells are proliferating, an increase in the number of tyrosine hydroxylase immunopositive  
35 neurons would represent an increase in the number of dopaminergic neurons surviving in vitro. Therefore, if a polypeptide of the invention acts to prolong the

survival of dopaminergic neurons, it would suggest that the polypeptide may be involved in Parkinson's Disease.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

10

**Example 37 - Inhibition of PDGF-induced Vascular Smooth Muscle Cell Proliferation Stimulatory Effect**

HAoSMC proliferation can be measured, for example, by BrdUrd incorporation. Briefly, subconfluent, quiescent cells grown on the 4-chamber slides 15 are transfected with CRP or FITC-labeled AT2-3LP. Then, the cells are pulsed with 10% calf serum and 6 mg/ml BrdUrd. After 24 h, immunocytochemistry is performed by using BrdUrd Staining Kit (Zymed Laboratories). In brief, the cells are incubated with the biotinylated mouse anti-BrdUrd antibody at 4 degrees C for 2 h after being exposed to denaturing solution and then incubated with the streptavidin-peroxidase 20 and diaminobenzidine. After counterstaining with hematoxylin, the cells are mounted for microscopic examination, and the BrdUrd-positive cells are counted. The BrdUrd index is calculated as a percent of the BrdUrd-positive cells to the total cell number. In addition, the simultaneous detection of the BrdUrd staining (nucleus) and the FITC 25 uptake (cytoplasm) is performed for individual cells by the concomitant use of bright field illumination and dark field-UV fluorescent illumination. See, Hayashida et al., J. Biol. Chem. 6:271(36):21985-21992 (1996).

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

30

**Example 38 - Effect of Polypeptides of the Invention on Cord Formation in Angiogenesis**

Another step in angiogenesis is cord formation, marked by differentiation of 35 endothelial cells. This bioassay measures the ability of microvascular endothelial cells to form capillary-like structures (hollow structures) when cultured in vitro.

CADMEC (microvascular endothelial cells) are purchased from Cell

5 Applications, Inc.' as proliferating (passage 2) cells and are cultured in Cell Applications' CADMEC Growth Medium and used at passage 5. For the in vitro angiogenesis assay, the wells of a 48-well cell culture plate are coated with Cell Applications' Attachment Factor Medium (200 ml/well) for 30 min. at 37°C. CADMEC are seeded onto the coated wells at 7,500 cells/well and cultured overnight  
10 in Growth Medium. The Growth Medium is then replaced with 300 mg Cell Applications' Chord Formation Medium containing control buffer or a polypeptide of the invention (0.1 to 100 ng/ml) and the cells are cultured for an additional 48 hr. The numbers and lengths of the capillary-like chords are quantitated through use of the Boeckeler VIA-170 video image analyzer. All assays are done in triplicate.

15 Commercial (R&D) VEGF (50 ng/ml) is used as a positive control. b-estradiol (1 ng/ml) is used as a negative control. The appropriate buffer (without protein) is also utilized as a control.

20 One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

25 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both  
30 incorporated herein by reference in their entireties.

## 5 CLAIMS

## WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 96.7% identical to a sequence selected from the group consisting of:
  - 10 (a) a polynucleotide fragment of SEQ ID NO:3 or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No: PTA-2966, which is hybridizable to SEQ ID NO:3;
  - (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:4 or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No: 15 PTA-2966, which is hybridizable to SEQ ID NO:3;
  - (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:4 or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No: PTA-2966, which is hybridizable to SEQ ID NO:3;
  - (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:4 or a 20 polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No: PTA-2966, which is hybridizable to SEQ ID NO:3;
  - (e) a polynucleotide encoding a polypeptide of SEQ ID NO:4 or the cDNA sequence included in ATCC Deposit No: PTA-2966, which is hybridizable to SEQ ID NO:3, having glycine receptor activity;
  - 25 (f) a polynucleotide which is a variant of SEQ ID NO:3;
  - (g) a polynucleotide which is an allelic variant of SEQ ID NO:3;
  - (h) an isolated polynucleotide comprising nucleotides 4 to 1293 of SEQ ID NO:3, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 431 of SEQ ID NO:4 minus the start codon;
  - 30 (i) an isolated polynucleotide comprising nucleotides 1 to 1293 of SEQ ID NO:3, wherein said nucleotides encode a polypeptide corresponding to amino acids 1 to 431 of SEQ ID NO:4 including the start codon;
  - (j) a polynucleotide which represents the complimentary sequence (antisense) of SEQ ID NO:3; and
  - 35 (k) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j), wherein said polynucleotide

5            does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2.        The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a human glycine receptor protein.

10        3.        A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

4.        A recombinant host cell comprising the vector sequences of claim 3.

5.        An isolated polypeptide comprising an amino acid sequence at least 96.2% identical to a sequence selected from the group consisting of:

15        (a) a polypeptide fragment of SEQ ID NO:4 or the encoded sequence included in ATCC Deposit No: PTA-2966;

              (b) a polypeptide fragment of SEQ ID NO:4 or the encoded sequence included in ATCC Deposit No: PTA-2966, having glycine receptor activity;

              (c) a polypeptide domain of SEQ ID NO:4 or the encoded sequence included

20        in ATCC Deposit No: PTA-2966;

              (d) a polypeptide epitope of SEQ ID NO:4 or the encoded sequence included in ATCC Deposit No: PTA-2966;

              (e) a full length protein of SEQ ID NO:4 or the encoded sequence included in ATCC Deposit No: PTA-2966;

25        (f) a variant of SEQ ID NO:4;

              (g) an allelic variant of SEQ ID NO:4;

              (h) a species homologue of SEQ ID NO:4;

              (i) a polypeptide comprising amino acids 2 to 431 of SEQ ID NO:4, wherein said amino acids 2 to 431 comprise a polypeptide of SEQ ID NO:4 minus the start

30        methionine;

              (j) a polypeptide comprising amino acids 1 to 431 of SEQ ID NO:4;

              (k) a polypeptide encoded by the cDNA contained in ATCC Deposit No. PTA-2966; and

              (l) a polypeptide comprising the polypeptide sequence of SEQ ID NO:74;

5        6. The isolated polypeptide of claim 5, wherein the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

7. An isolated antibody that binds specifically to the isolated polypeptide of claim 5.

10      8. A recombinant host cell that expresses the isolated polypeptide of claim 5.

9. A method of making an isolated polypeptide comprising:

      (a) culturing the recombinant host cell of claim 8 under conditions such that said polypeptide is expressed; and

15      (b) recovering said polypeptide.

10. The polypeptide produced by claim 9.

11. A method for preventing, treating, or ameliorating a medical condition, comprising the step of administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 5 or the polynucleotide of claim 1.

20      12. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

      (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

      (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

25      13. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

      (a) determining the presence or amount of expression of the polypeptide of claim 5 in a biological sample; and

30      (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

14. An isolated nucleic acid molecule consisting of a polynucleotide having a nucleotide sequence selected from the group consisting of:

35      (a) a polynucleotide encoding a polypeptide of SEQ ID NO:2;

5 (b) an isolated polynucleotide consisting of nucleotides 4 to 1251 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 417 of SEQ ID NO:2 minus the start codon;

(c) an isolated polynucleotide consisting of nucleotides 1 to 1251 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 1 to 417 of SEQ ID NO:2 including the start codon;

10 (d) a polynucleotide which represents the complimentary sequence (antisense) of SEQ ID NO:2;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:4;

(f) an isolated polynucleotide consisting of nucleotides 4 to 1293 of 15 SEQ ID NO:3, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 431 of SEQ ID NO:4 minus the start codon;

(g) an isolated polynucleotide consisting of nucleotides 1 to 1293 of SEQ ID NO:3, wherein said nucleotides encode a polypeptide corresponding to amino acids 1 to 431 of SEQ ID NO:2 including the start codon;

20 (h) a polynucleotide encoding the HGRAsv polypeptide encoded by the cDNA clone contained in ATCC Deposit No. PTA-2966; and

(i) a polynucleotide which represents the complimentary sequence (antisense) of SEQ ID NO:4.

15. The isolated nucleic acid molecule of claim 14, wherein the 25 polynucleotide comprises a nucleotide sequence encoding a human glycine receptor protein.

16. A recombinant vector comprising the isolated nucleic acid molecule of claim 14.

17. A recombinant host cell comprising the recombinant vector of claim 30 16.

18. An isolated polypeptide consisting of an amino acid sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:2 having glycine receptor activity;

35 (b) a polypeptide domain of SEQ ID NO:2 having glycine receptor activity;

5 (c) a full length protein of SEQ ID NO:2;

(d) a polypeptide corresponding to amino acids 2 to 417 of SEQ ID NO:2, wherein said amino acids 2 to 417 comprise a polypeptide of SEQ ID NO:2 minus the start methionine;

(e) a polypeptide corresponding to amino acids 1 to 417 of SEQ ID NO:2;

10 (f) a polypeptide fragment of SEQ ID NO:4 having glycine receptor activity;

(g) a polypeptide domain of SEQ ID NO:4 having glycine receptor activity;

(h) a full length protein of SEQ ID NO:4;

15 (i) a polypeptide corresponding to amino acids 2 to 431 of SEQ ID NO:4, wherein said amino acids 2 to 431 comprise a polypeptide of SEQ ID NO:4 minus the start methionine;

(j) a polypeptide corresponding to amino acids 1 to 431 of SEQ ID NO:4; and

20 (k) a polypeptide encoded by the cDNA contained in ATCC Deposit No. PTA-2966.

19. The method for preventing, treating, or ameliorating a medical condition of claim 11, wherein the medical condition is a disorder selected from the group consisting of: neural disorder, a neural disorder related to aberrant excitotoxic cell death, a neural disorder related to chronic peripheral neuropathies, a gastrointestinal disorder, a gastrointestinal disorder related to aberrant longitudinal muscle/myenteric plexus contractions, irritable bowel syndrome, a disorder related to hyper glycine receptor activity.

25

Figure 1A

1	ATGACAACTCTTGTTCCTGCAACCCCTCCCTCCTCTCTGGACCTGCCAGGGCAG	60
1	M T T L V P A T L S F L L L W T L P G Q	20
61	GTCCTCCTCAGGGTGGCCTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGTCCCAG	120
21	V L L R V A L A K E E V K S G T K G S Q	40
121	CCCATGTCCCCCTCTGATTTCCTAGACAAACTATGGGGCGAACATCTGGATATGATGCC	180
41	P M S P S D F L D K L M G R T S G Y D A	60
181	AGGATTGGGCCAATTTAAAGGCCACCGTGAACGTGACCTGCAACATCTCATCAAC	240
61	R I R P N F K G P P V N V T C N I F I N	80
241	AGTTTCAGCTCCGTACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTGCGGCAA	300
81	S F S S V T K T T M D Y R V N V F L R Q	100
301	CAGTGGAAATGACCCACGCCTGTCCTACCGAGAAATATCCTGATGACTCTGGACCTCGAT	360
101	Q W N D P R L S Y R E Y P D D S L D L D	120
361	CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTGCTAATGAGAAAGGGCC	420
121	P S M L D S I W K P D L F F A N E K G A	140
421	AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTCAAGAAATGGGAATGTG	480
141	N F H E V T T D N K L L R I F K N G N V	160
481	CTGTACAGCATCAGGCTGACCTCATTTGTCCTGCCTGATGGACCTCAAGAACCTCCC	540
161	L Y S I R L T L I L S C L M D L K N F P	180
541	ATGGACATCCAGACCTGCACGATGCAGCTTGAGAGCTTGGCTACACCATGAAAGACCTC	600
181	M D I Q T C T M Q L E S <b>E G Y</b> T M K D L	200
601	GTGTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGCTGACTCTGCC	660
201	V F E W L E D A P A V Q V A E G L T L P	220
661	CAGTTTATCTTGCAGGATGAGAAGGATCTAGGCTGTTGCTACCAAGCACTACAACACAGGG	720
221	Q F I L R D E K D L G C C T <b>E R Y P G</b>	240
721	AAATTACCTGCATCGAGGTAAAGTTCACCTGGAACGGCAGATGGCTACTATCTGATT	780
241	K F T C I E V K F H L E R Q <u>M G Y Y L I</u>	260
781	CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGCTGGGTCTCCTCTGGATCAAC	840
261	<u>O M Y I P S L L I V I L S W V S F W I N</u>	280
841	ATGGATGCTGCCCTGCCGTGTGGCCTGGGCATCACCAACCGTGCTCACCATGACCACC	900
281	<u>M D A A P A R V G L G I T T V L T M T T</u>	300

## Figure 1B

901	CAGAGCTCTGGCTCCGGGCTCTTGCTAAGGTGCTTACGTGAAGGCAATCGACATC	960
301	<u>Q S S G S R A S L P K V S Y V K A I D I</u>	320
961	TGGATGGCTGTGTCTGCTCTTGCTGCTGCCCTGCTGGAGTATGCTGCCATAAAT	1020
321	<u>W M A V C L L F V F A A L L E Y A A I N</u>	340
1021	TTTGTTCCTCGTCAGCATAAAGAATTACATACGACTTCGAAGAAGGCAGAGGCCAACGC	1080
341	<u>F V S R Q H K E F I R L R R R Q R R Q R</u>	360
1081	TTGGAGGAAGATATCATCCAAGAAAGTCGTTCTATTCCGTGGCTATGGCTGGCAC	1140
361	<u>L E E D I I Q E S R F Y F R G Y G L G H</u>	380
1141	TGCCTGCAGGCAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCT	1200
381	<u>C L Q A R D G G P M E G S G I Y S P Q P</u>	400
1201	CCAGCCCTCTAAGGAAGGAGAAACCACGCGAAACTCTACGTGGACTGAGCCAAG	1260
401	<u>P A P L L R E G E T T R K L Y V D</u>	417
1261	AGAATTGACACCATCTCCGGGCTGTCTCCCTTCACTTCCATCTTCATATCTTC	1320
1321	TACTGGGTTGTCTATAAAAGTGCCTACGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGG	1380
1381	TGGGAGCTATAGAGTCCTGCTGCTGGCCTCCTGCTCCCTGGTGGCTTCTCCCTC	1440
1441	AGTTAGACTCCATTAGGGTTGGACAGTCCTCCTGATCTCCACTCAGAACTTCAAC	1500
1501	TACCACTCCAAAGCTATGTGGCCTATATTGCATGGTGCCTGGCTGTACTTATA	1560
1561	AAGATGGCTTATCTACCCCTAGTCATATTCTCCATACTTCCATTTCATGAGACT	1620
1621	AAGGTTGCCACATTCCCTGGGCCAGGATGACCTCTGCCCTGCTGGAGCCTCCGT	1680
1681	TTTCCAATACTCCAGTGGAGAGTATTCAAGAACACTGCTGCTAGATTCTGGCATTGTCAT	1740
1741	CTTAATCTGCACCACTCTCCCCCTGCCACCTCCACCCAGAGCCTGGCATTACTCTGT	1800
1801	CCTCTGTCCCTCCTGCTGCAGATTCAAATGGTGAGTTCTCTATCCACAAGTGCTGCC	1860
1861	TGTGGGCCCTAGTCAGGTTCTGAAGTGAGAGGAAGGCAAAGCCGCAAGTTCCCCACC	1920
1921	TCTCGAGAGGGTTGGAACAGTCATAGGCTGCACTGGCTAGCGACTATATGGCCCAACAG	1980

**Figure 1C**

1981	AGAGGTGTTCAAGTCTCTGGGAAGCCCCACACTTGTCTTCATCCCTTCCTATTGCG	2040
2041	CTTGTCTGCTCTTCCTGTTCACTGAGATACTCCTTTGTCTGTCTTAGTTGAGGA	2100
2101	GAGCGTTCTGAGCTGACCAGGGTAGCTGGTCAGAAATTACTGTCAGAATTGGGGCAGAG	2160
2161	ACTTTGGTTCTCAAAAAGACTAACCTCCAGATCCACCTGAACATTCTGGTCTCAGAAA	2220
2221	TATTCGTTCCGTTCCCTAATTAACCTAGCATGGTGGCAGGATCTGTTGGACAGCTGGGAG	2280
2281	TGTAAAAAAAGAAAAATACTTGTCTTTAAGAAACTTACTTTATGATGCTAGAAAAC	2340
2341	TGAGAAAAGTGAGATCCAAGGTAGTGGAACCCAGGAGGAGTAGAATAGAGAAACTATTCT	2400
2401	CAGAGTGTCTTTGTTGGCTGGCTTCATTTGTTCTTCACCAAAGTCTATT	2460
2461	TCCAGGGCCCTCATTTCAACCTGGTCTTCACCTCCTTGGTGTGCAAATAAGGTG	2520
2521	CCGCTGCAACCTGTTAAGGATAAAAAAAAAAAAAAAAAAAAAA	2565

Figure 2A

1	ATGACAACTCTTGTCTGCCAACCTCTCCTCTTCTCTGGACCCGCCAGGGCAG	60
1	M T T L V P A T L S F L L L W T L P G Q	20
61	GTCCTCCTCAGGGTGGCCTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGTCCCAG	120
21	V L L R V A L A K E E V K S G T K G S Q	40
121	CCCATGTCCCCCTCTGATTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC	180
41	P M S P S D F L D K L M G R T S G Y D A	60
181	AGGATTGGGCCAATTTAAAGGCCACCGTGAACGTGACCTGCAACATCTCATCAAC	240
61	R I R P N F K G P P V N V T C N I F I N	80
241	AGTTTCAGCTCCGTACCAAGACCACAATGGACTACCGGGTGAATGTCTTGCAGGCAA	300
81	S F S S V T K T T M D Y R V N V F L R Q	100
301	CAGTGGAAATGACCCACGCCCTGTCCTACCGAGAAATATCCTGATGACTCTGGACCTCGAT	360
101	Q W N D P R L S Y R E Y P D D S L D L D	120
361	CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTGCTAATGAGAAAGGGCC	420
121	P S M L D S I W K P D L F F A N E K G A	140
421	AACTTCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGAAATGTG	480
141	N F H E V T T D N K L L R I F K N G N V	160
481	CTGTACAGCATCAGGCTGACCCCTCATTTGTCCTGCCTGATGGACCTCAAGAACTTCCC	540
161	L Y S I R L T L I L S C L M D L K N F P	180
541	ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG	600
181	M D I Q T C T M Q L E S S S I L C S P L	200
601	CCATCTGTCACTTCAGTTGGCTACACCATGAAAGACCTCGTGTGAGTGGCTGGAA	660
201	P S L S L S V <del>■■■■■</del> T M K D L V F E W L E	220
661	GATGCTCCTGCTGCCAAGTGGCTGAGGGCTGACTCTGCCAGTTATCTGGGGAT	720
221	D A P A V Q V A E G L T L P Q F I L R D	240
721	GAGAAGGATCTAGGCTGTTGACCAAGCACTACAACACAGGGAAATTCAACCTGCATCGAG	780
241	E K D L G C C T <del>■■■■■</del> G K F T C I E	260
781	GTAAAGTTCACCTGGAACGGCAGATGGCTACTATCTGATTGAGATGTACATCCCCAGC	840
261	V K F H L E R Q <u>M G Y Y</u> L I O M Y I P S	280
841	CTACTCATCGTCATCCTGTCCTGGGTCTCCTCTGGATCAACATGGATGCTGCCCTGCC	900
281	<u>L L I V I L S W V S F W I N M</u> D A A P A	300

## Figure 2B

901	CGTGTGGGCTGGCATCACCAACCGTGCACCATGACCACCCAGAGCTCTGGCTCCCGG	960
301	R <u>V G L G I T T V L T M T T Q S S G S R</u>	320
961	GCCTCTTGCCTAACGGTGTCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTCTG	1020
321	A S L P K V S Y V K A I D <u>I W M A V C L</u>	340
1021	CTCTTGTTGCTGCCTGGAGTATGCTGCCATAATTGTTCTCGTCAGCAT	1080
341	<u>L F V F A A L L E Y A A I N F V S R Q H</u>	360
1081	AAAGAATTCAACGACTTCGAAGAAGGCAGAGGCCAACGCTGGAGGAAGATATCATC	1140
361	K E F I R L R R R Q R R Q R L E E D I I	380
1141	CAAGAAAGTCGTTCTATTCCGTGGCTATGGCTGGCCACTGCCTGCAGGCAAGAGAT	1200
381	Q E S R F Y F R G Y G L G H C L Q A R D	400
1201	GGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCTCCAGCCCTCTAAGG	1260
401	G G P M E G S G I Y S P Q P P A P L L R	420
1261	GAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC	1320
421	E G E T T R K L Y V D	431
1321	CGGGCTGTCTCCCTTCACTTCCCTCATCTTCAATATCTTCTACTGGGTGTCTATAAAA	1380
1381	GTGCTATGGTCAGAAGATATCCACCAAGGCTCTGTGAATAGGGTGGGAGCTATAGACTCCT	1440
1441	GCTGCTGGCCTCCTGCTCCTGGTGGCTTCTCCCTCAGTTAGACTCCATTAGGG	1500
1501	GTGGGACAGTCCTCCTGATCTCCCCTCAGAACTCAACTACCAGTCCAAAGCTAT	1560
1561	GTGGGCCTATATTGCATGGTGCCAATGGTGGCTGTACTTATAAAGATGGCTTATCTACCC	1620
1621	TAAAAAAAAAAAAAAAAA 1640	

Figure 3A

	1	50
GRA1_HUMAN	(1)	-----MYSFNTLRLYLSGAIYFSLAASKAFAAARSATKPMSPSDFLDK
GRA3_HUMAN	(1)	-MAHVRHFRILVSGFYWEAALLSLVATTEDESARSAPMSPDFLDK
HGRA4	(1)	MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGIKGSQPMSPSDFLDK
HGRA4sv	(1)	MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGIKGSQPMSPSDFLDK
GRA4_MOUSE	(1)	-----VALAKEDVKSGLKGSQPMSPSDFLDK
GRA2_HUMAN	(1)	MNROIWNLHALFALFLETNHERTAFCKDHDPSRSCKQPSQTMSPSDFLDK
	51	100
GRA1_HUMAN	(45)	LMGRTSGYDARIRPNFKGPPVNVCNIFINSFGSIAETTMDYRVNMFRLQ
GRA3_HUMAN	(50)	LMGRTSGYDARIRPNFKGPPVNVCNIFINSFGSIAETTMDYRVNMFRLQ
HGRA4	(51)	LMGRTSGYDARIRPNFKGPPVNVCNIFINSFGSIAETTMDYRVNMFRLQ
HGRA4sv	(51)	LMGRTSGYDARIRPNFKGPPVNVCNIFINSFGSIAETTMDYRVNMFRLQ
GRA4_MOUSE	(27)	LMGRTSGYDARIRPNFKGPPVNVCNIFINSFGSIAETTMDYRVNMFRLQ
GRA2_HUMAN	(51)	LMGRTSGYDARIRPNFKGPPVNVCNIFINSFGSIAETTMDYRVNMFRLQ
	101	150
GRA1_HUMAN	(95)	QWNPDPRLAYNEYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
GRA3_HUMAN	(100)	QWNPDPRLAYSEYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
HGRA4	(101)	QWNPDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
HGRA4sv	(101)	QWNPDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
GRA4_MOUSE	(77)	QWNPDPRLAYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
GRA2_HUMAN	(101)	QWNDSRLAYSEYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
	151	200
GRA1_HUMAN	(145)	LLRISRNGNVLYSIRTLTLACEMDLKNFPMDVOTCIMQLES-----
GRA3_HUMAN	(150)	LLRIFKNGNVLYSIRTLTLSCMDLKNFPMDVOTCIMQLES-----
HGRA4	(151)	LLRIFKNGNVLYSIRTLTLSCMDLKNFPMDVOTCIMQLES-----
HGRA4sv	(151)	LLRIFKNGNVLYSIRTLTLSCMDLKNFPMDVOTCIMQLESSSIILCSPL
GRA4_MOUSE	(127)	LLRIFKNGNVLYSIRTLTLSCMDLKNFPMDVOTCIMQLES-----
GRA2_HUMAN	(151)	LLRISKNGKVLYSIRTLTLSCMDLKNFPMDVOTCIMQLES-----
	201	250
GRA1_HUMAN	(187)	-----FGYTMNDLIFEWQE@GA-VQVAEGTLTPQFILKEEKDILRYCTKH
GRA3_HUMAN	(192)	-----FGYTMNDLIFEWQEDAP-VQVAEGTLTPQFILKEEKDILRYCTKH
HGRA4	(193)	-----FGYTMNDLIFEWLEDAPAVQVAEGTLTPQFILRDEKDLIGCCTKH
HGRA4sv	(201)	PSLSLSVGYTMNDLIFEWLEDAPAVQVAEGTLTPQFILRDEKDLIGCCTKH
GRA4_MOUSE	(169)	-----FGYTMNDLIFEWLEDAPAVQVAEGTLTPQFILRDEKDLIGYCTKH
GRA2_HUMAN	(193)	-----FGYTMNDLIFEWLDGAP-VQVAEGTLTPQFILKEEKELGYCTKH
	251	300
GRA1_HUMAN	(230)	[<<<<<<<<TM1>>>>>>>>>] YNTGKFTCIEAFHLERQMGYYLIQMYIPSSLIVILSWVSFWINMDAAPA
GRA3_HUMAN	(235)	YNTGKFTCIEVAFHLERQMGYYLIQMYIPSSLIVILSWVSFWINMDAAPA
HGRA4	(237)	YNTGKFTCIEVKFHLLERQMGYYLIQMYIPSSLIVILSWVSFWINMDAAPA
HGRA4sv	(251)	YNTGKFTCIEVKFHLLERQMGYYLIQMYIPSSLIVILSWVSFWINMDAAPA
GRA4_MOUSE	(213)	YNTGKFTCIEVKFHLLERQMGYYLIQMYIPSSLIVILSWVSFWINMDAAPA
GRA2_HUMAN	(236)	YNTGKFTCIEVKFHLLERQMGYYLIQMYIPSSLIVILSWVSFWINMDAAPA
	3[<<<<<<<TM2>>>>>]	[<<<<<<<<<TM3
GRA1_HUMAN	(280)	RVGLGITTVLMTTQSSGRASLPKVSYVKAIDIWMAVCLJFVF <del>A</del> LEY
GRA3_HUMAN	(285)	RVALGITTVLMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVF <del>A</del> LEY
HGRA4	(287)	RVGLGITTVLMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVF <del>A</del> LEY
HGRA4sv	(301)	RVGLGITTVLMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVF <del>A</del> LEY
GRA4_MOUSE	(263)	RVGLGITTVLMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVF <del>A</del> LEY
GRA2_HUMAN	(286)	RVALGITTVLMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVF <del>A</del> LEY

Figure 3B

	>>>>>]	400
GRA1_HUMAN	(330) AAVNFVSRQHKEFLRLRRRQR-----	AAKEDAEAGEGRFNFS
GRA3_HUMAN	(335) AAVNFVSRQHKEFLRLRRRQR-----	AAKTEAFALEKFYRFSDMIDEVRESRFSFI
HGRA4	(337) AAINFVSRQHKEFIRLRRRQR-----	RQRLEEDIIQESRFYFR
HGRA4sv	(351) AAINFVSRQHKEFIRLRRRQR-----	RQRLEEDIIQESREYFR
GRA4_MOUSE	(313) AAVNFVSRQXKEFIRLRRRQR-----	RQRW-----
GRA2_HUMAN	(336) AAVNFVSRQHKEFLRLRRRQR-----	RONKEEDVIRESRFNFS
	401	450
GRA1_HUMAN	(366) AYGMGPACLQAKDGISVKGANNSTINPPPAPSKSPEEMRKLFIGRAKKI	
GRA3_HUMAN	(385) AYGMGP-CLQAKDGMTPKGPN-----	HPVQVMPKSPDEEMRKVFTDRAKKI
HGRA4	(375) GYGIGH-CLQAKDGPPMEGS-GIYSPQPPAPMIREGETTRKLWVD-----	
HGRA4sv	(389) GYGIGH-CLQAKDGPPMEGS-GIYSPQPPAPMIREGETTRKLWVD-----	
GRA4_MOUSE	(338) -----	
GRA2_HUMAN	(374) GYGMGH-CLQAKDGTAVKATPANPLPQPPK-----	DGDAIKKKFVDRAKRI
	451	487
GRA1_HUMAN	(416) DKISRIGFPMAFLIFNMFYWIIYKIDRREDVHNQ---	
GRA3_HUMAN	(429) DTISRACFPMAFLIFNMFYWIIYKIDRHEDVHHQQD	
HGRA4	(418) -----	
HGRA4sv	(432) -----	
GRA4_MOUSE	(338) -----	
GRA2_HUMAN	(419) DTISRAAFFPMAFLIFNMFYWIIYKIDRHEDVHKK---	

Figure 4

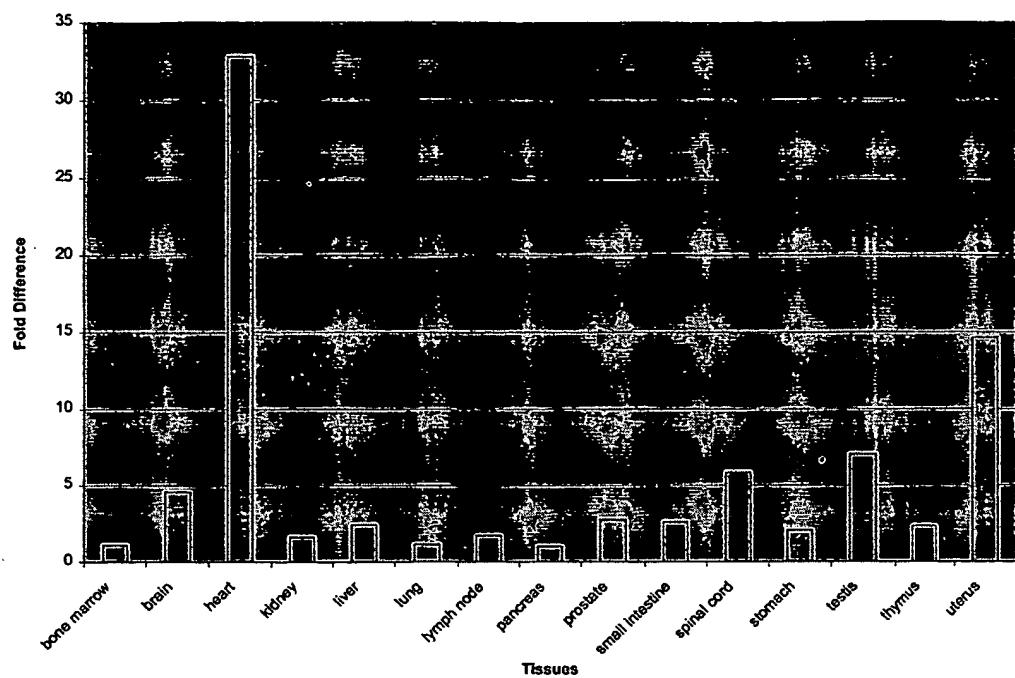


Figure 5

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 cloneE3 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRSGYDA  
 cloned8 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRSGYDA  
 \*\*\*\*\*

G1934909\_001 RIRPNFKGPPVNVCNIFINSFSSITKTTMACWAPGNGNVSEGPIAPSQDYRVNVFLRQ  
 cloneE3 RIRPNFKGPPVNVCNIFINSFSSVTKTTM-----DYRVNVFLRQ  
 cloned8 RIRPNFKGPPVNVCNIFINSFSSVTKTTM-----DYRVNVFLRQ  
 \*\*\*\*\*

G1934909\_001 QWNPDPLSYREYPDDSLDLPSPMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV  
 cloneE3 QWNPDPLSYREYPDDSLDLPSPMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV  
 cloned8 QWNPDPLSYREYPDDSLDLPSPMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV  
 \*\*\*\*\*

G1934909\_001 LYSIRLTLILSCLMDLKNFPMDIQTCTMQLES-----FGYTMKDLVFEWLE  
 cloneE3 LYSIRLTLILSCLMDLKNFPMDIQTCTMQLES-----FGYTMKDLVFEWLE  
 cloned8 LYSIRLTLILSCLMDLKNFPMDIQTCTMQLLESSSSILCSPPLSLSVGYTMKDLVFEWLE  
 \*\*\*\*\*

G1934909\_001 DAPAVQVAEGLTLPQFILRDEKDLGCTKHYNTGKFTCIEVKFHLEQMGYYLIQMYIPS  
 cloneE3 DAPAVQVAEGLTLPQFILRDEKDLGCTKHYNTGKFTCIEVKFHLEQMGYYLIQMYIPS  
 cloned8 DAPAVQVAEGLTLPQFILRDEKDLGCTKHYNTGKFTCIEVKFHLEQMGYYLIQMYIPS  
 \*\*\*\*\*

G1934909\_001 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGRASLPK-----  
 cloneE3 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGRASLPKVSYVKAIIDIWMAVCL  
 cloned8 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGRASLPKVSYVKAIIDIWMAVCL  
 \*\*\*\*\*

G1934909\_001 -----  
 cloneE3 LFVFAALLEYAAINFVSRQHKEFIRLRRRQRQRLEEDIIQESRFYFRGYGLGHCLQARD  
 cloned8 LFVFAALLEYAAINFVSRQHKEFIRLRRRQRQRLEEDIIQESRFYFRGYGLGHCLQARD

G1934909\_001 -----  
 cloneE3 GGPMEGSGIYSPQPPAPLLREGETTRKLYVD  
 cloned8 GGPMEGSGIYSPQPPAPLLREGETTRKLYVD

**Figure 6.****HGRA4**

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.8%	82.2%
human glycine receptor alpha 3 subunit	gi 5729844	84.4%	78.7%
mouse glycine receptor subunit alpha 4 protein	gi 817957	97%	96%
human glycine receptor alpha 2 subunit	gi 4504021	80.6%	86.5%

**HGRA4sv**

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.5%	82%
human glycine receptor alpha 3 subunit	gi 5729844	78.5%	84.2%
mouse glycine receptor subunit alpha 4 protein	gi 817957	95.8%	96.7%
human glycine receptor alpha 2 subunit	gi 4504021	80.3%	86.2%

**Figure 7**

Atgacaactcttgtcctgcaacccttccttccttcgtggaccctgccagggcaggtcctcctcagggtggcct  
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Figure 8

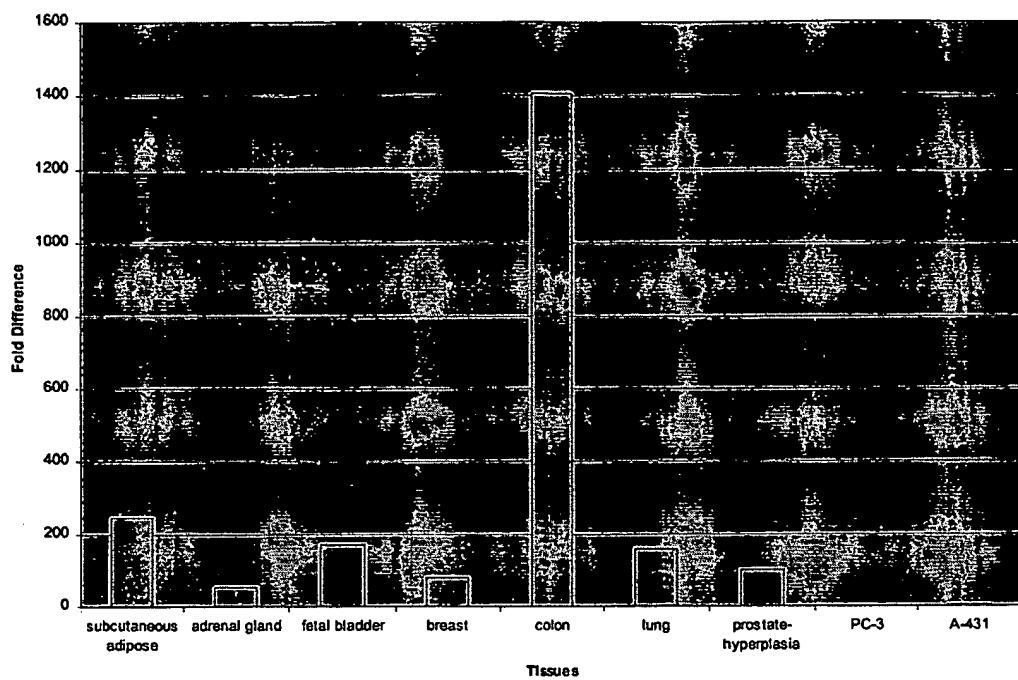


Figure 9



## SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT EXPRESSED IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF

<130> D0079 PCT

<150> US 60/269,535

<151> 2001-02-16

<160> 81

<170> PatentIn version 3.0

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Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val  
20 25 30

96

aaa tct gga acc aag ggg tcc cag ccc atg tcc ccc tct gat ttc cta  
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192

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336

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384

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Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser	
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Lys Phe Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly	
245 250 255	
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260 265 270	
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aaaa 2565

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<211> 417  
<212> PRT  
<213> homo sapiens

<400> 2

Met Thr Thr Leu Val Pro Ala Thr Leu Ser Phe Leu Leu Leu Trp Thr  
1 5 10 15

Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val  
20 25 30

Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu  
35 40 45

Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro  
50 55 60

Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn  
65 70 75 80

Ser Phe Ser Ser Val Thr Lys Thr Met Asp Tyr Arg Val Asn Val  
85 90 95

Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr  
100 105 110

Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp  
115 120 125

Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Gly Ala Asn Phe His Glu  
130 135 140

Val Thr Thr Asp Asn Lys Leu Leu Arg Ile Phe Lys Asn Gly Asn Val  
145 150 155 160

Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu Ser Cys Leu Met Asp Leu  
165 170 175

Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser  
180 185 190

Phe Gly Tyr Thr Met Lys Asp Leu Val Phe Glu Trp Leu Glu Asp Ala  
195 200 205

Pro Ala Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu  
210 215 220

Arg Asp Glu Lys Asp Leu Gly Cys Cys Thr Lys His Tyr Asn Thr Gly  
225 230 235 240

Lys Phe Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly  
245 250 255

Tyr Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu  
260 265 270

Ser Trp Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val  
275 280 285

Gly Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly  
290 295 300

Ser Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile  
305 310 315 320

Trp Met Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr  
325 330 335

Ala Ala Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu  
340 345 350

Arg Arg Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu  
355 360 365

Ser Arg Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala  
370 375 380

Arg Asp Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro  
385 390 395 400

Pro Ala Pro Leu Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val  
405 410 415

Asp

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<210> 3
<211> 1640
<212> DNA
<213> homo sapiens
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<220>  
<221> CDS  
<222> (1)..(1293)

<400> 3  
atg aca act ctt gtt cct gca acc ctc tcc ttc ctt ctt ctc tgg acc 48  
Met Thr Thr Leu Val Pro Ala Thr Leu Ser Phe Leu Leu Leu Trp Thr  
1 5 10 15

ctg cca ggg cag gtc ctc ctc agg gtg gcc ttg gca aaa gag gaa gtc 96  
 Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val  
 20 25 30

```

aaa tct gga acc aag ggg tcc cag ccc atg tcc ccc tct gat ttc cta      144
Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu
            35          40          45

```

```

gac aaa ctt atg ggg cga aca tct gga tat gat gcc agg att cgg ccc      192
Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro
      50          55          60

```

```

aat ttt aaa ggc cca ccc gtg aac gtg acc tgc aac atc ttc atc aac      240
Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn
65          70          75          80

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agt ttc agc tcc gtc acc aag acc aca atg gac tac cgg gtg aat gtc 288  
 Ser Phe Ser Ser Val Thr Lys Thr Thr Met Asp.Tyr Arg Val Asn Val  
 85 90 95

ttc ttg cg<sup>g</sup> caa cag tgg aat gac cca cgc ctg tcc tac cga gaa tat 336  
 Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr  
 100 105 110

cct gat gac tct ctg gac ctc gat ccc tcc atg ctg gac tct atc tgg 384  
Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp  
115 120 125

```

aag cca gac ctc ttc ttt gct aat gag aaa ggg gcc aac ttc cat gag 432
Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Gly Ala Asn Phe His Glu
    130          135          .          140

```

gtg acc acg gac aac aag tta ctg cgc atc ttc aag aat ggg aat gtg 480  
 Val Thr Thr Asp Asn Lys Leu Leu Arg Ile Phe Lys Asn Gly Asn Val

145	150	155	160	
ctg tac agc atc agg ctg acc ctc att ttg tcc tgc ctg atg gac ctc				528
Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu Ser Cys Leu Met Asp Leu				
165	170	175		
aag aac ttc ccc atg gac atc cag acg tgc acg atg cag ctt gag agc				576
Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser				
180	185	190		
tca tcc ata ctc tgc agc cct ctg cca tct ctg tca ctt tca gtt ggc				624
Ser Ser Ile Leu Cys Ser Pro Leu Pro Ser Leu Ser Leu Ser Val Gly				
195	200	205		
tac acc atg aaa gac ctc gtg ttt gag tgg ctg gaa gat gct cct gct				672
Tyr Thr Met Lys Asp Leu Val Phe Glu Trp Leu Glu Asp Ala Pro Ala				
210	215	220		
gtc caa gtg gct gag ggg ctg act ctg ccc cag ttt atc ttg cggt gat				720
Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu Arg Asp				
225	230	235	240	
gag aag gat cta ggc tgt tgt acc aag cac tac aac aca ggg aaa ttc				768
Glu Lys Asp Leu Gly Cys Cys Thr Lys His Tyr Asn Thr Gly Lys Phe				
245	250	255		
acc tgc atc gag gta aag ttt cac ctg gaa cggt cag atg ggc tac tat				816
Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly Tyr Tyr				
260	265	270		
ctg att cag atg tac atc ccc agc cta ctc atc gtc atc ctg tcc tgg				864
Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu Ser Trp				
275	280	285		
gtc tcc ttc tgg atc aac atg gat gct gcc cct gcc cgt gtg ggc ctg				912
Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val Gly Leu				
290	295	300		
ggc atc acc acc gtg ctc acc atg acc acc cag agc tct ggc tcc cggt				960
Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly Ser Arg				
305	310	315	320	
gcc tct ttg cct aag gtg tcc tac gtg aag gca atc gac atc tgg atg				1008
Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile Trp Met				
325	330	335		
gct gtg tgt ctg ctc ttt gtg ttc gct gcc ttg ctg gag tat gct gcc				1056
Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr Ala Ala				
340	345	350		
ata aat ttt gtt tct cgt cag cat aaa gaa ttc ata cga ctt cga aga				1104
Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu Arg Arg				
355	360	365		
agg cag agg cgc caa cgc ttg gag gaa gat atc atc caa gaa agt cgt				1152
Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu Ser Arg				
370	375	380		

ttc tat ttc cgt ggc tat ggc ttg ggc cac tgc ctg cag gca aga gat 1200  
 Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala Arg Asp  
 385 390 395 400

gga ggt cca atg gaa ggt tct ggc att tat agt ccc caa cct cca gcc 1248  
 Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro Pro Ala  
 405 410 415

cct ctt cta agg gaa gga gaa acc acg cgg aaa ctc tac gtg gac 1293  
 Pro Leu Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val Asp  
 420 425 430

ttagccaaga gaattgacac catctccgg gctgtttcc ctttcaactt cctcatcttc 1353  
 aatatcttct actgggttgt ctataaagtg ctatggtcag aagatatcca ccaggctctg 1413  
 tgaatagggt gggagctata gagtcctgct gctggctcc tgcttcctcc tgggtggct 1473  
 ttctccctca gttagactcc attaggggtt tggacagttc cttcctgatc tcccactcag 1533  
 aacttcaact accagtccca aagctatgtg ggcctatatt gcatggtgcc aatggggct 1593  
 gtacttataa agatggctta tctaccctaa aaaaaaaaaa aaaaaaaaa 1640

<210> 4  
 <211> 431  
 <212> PRT  
 <213> homo sapiens

<400> 4

Met Thr Thr Leu Val Pro Ala Thr Leu Ser Phe Leu Leu Leu Trp Thr  
 1 5 10 15

Leu Pro Gly Gln Val Leu Leu Arg Val Ala Leu Ala Lys Glu Glu Val  
 20 25 30

Lys Ser Gly Thr Lys Gly Ser Gln Pro Met Ser Pro Ser Asp Phe Leu  
 35 40 45

Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro  
 50 55 60

Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn  
 65 70 75 80

Ser Phe Ser Ser Val Thr Lys Thr Met Asp Tyr Arg Val Asn Val  
 85 90 95

Phe Leu Arg Gln Gln Trp Asn Asp Pro Arg Leu Ser Tyr Arg Glu Tyr  
100 105 110

Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp  
115 120 125

Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Gly Ala Asn Phe His Glu  
130 135 140

Val Thr Thr Asp Asn Lys Leu Leu Arg Ile Phe Lys Asn Gly Asn Val  
145 150 155 160

Leu Tyr Ser Ile Arg Leu Thr Leu Ile Leu Ser Cys Leu Met Asp Leu  
165 170 175

Lys Asn Phe Pro Met Asp Ile Gln Thr Cys Thr Met Gln Leu Glu Ser  
180 185 190

Ser Ser Ile Leu Cys Ser Pro Leu Pro Ser Leu Ser Leu Ser Val Gly  
195 200 205

Tyr Thr Met Lys Asp Leu Val Phe Glu Trp Leu Glu Asp Ala Pro Ala  
210 215 220

Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu Arg Asp  
225 230 235 240

Glu Lys Asp Leu Gly Cys Cys Thr Lys His Tyr Asn Thr Gly Lys Phe  
245 250 255

Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly Tyr Tyr  
260 265 270

Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu Ser Trp  
275 280 285

Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val Gly Leu  
290 295 300

Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly Ser Arg  
305 310 315 320

Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile Trp Met

325

330

335

Ala Val Cys Leu Leu Phe Val Phe Ala Ala Leu Leu Glu Tyr Ala Ala  
 340 345 350

Ile Asn Phe Val Ser Arg Gln His Lys Glu Phe Ile Arg Leu Arg Arg  
 355 360 365

Arg Gln Arg Arg Gln Arg Leu Glu Glu Asp Ile Ile Gln Glu Ser Arg  
 370 375 380

Phe Tyr Phe Arg Gly Tyr Gly Leu Gly His Cys Leu Gln Ala Arg Asp  
 385 390 395 400

Gly Gly Pro Met Glu Gly Ser Gly Ile Tyr Ser Pro Gln Pro Pro Ala  
 405 410 415

Pro Leu Leu Arg Glu Gly Glu Thr Thr Arg Lys Leu Tyr Val Asp  
 420 425 430

<210> 5  
 <211> 679  
 <212> DNA  
 <213> homo sapiens

<400> 5		
atatacgacg tagagctgct tagcatacat ctatctcatg agtagtgttg tgaccataaa	60	
aagcatgcaa tggccctgtg tacccaaggc accttgcgtc cataacattc cctatgagat	120	
attgatgggt ggtctgttct ctatccctct gcctttgagc tttgacactca aattctgccg	180	
tttcttcctt gtaattccag gaggaagata tcatccaaga aagtgcgttc tattccgtg	240	
gctatggctt gggccactgc ctgcaggcaa gagatggagg tccaatggaa gttctggca	300	
tttatagtcc ccaacctcca gccctcttc taagggaaagg agaaaccacg cgaaactct	360	
acgtggactg agccaagaga attgacacca tctccgggc tgtctccct ttcactttcc	420	
tcatcttcaa tatcttctac tgggtgtct ataaagtgtc atggtcagaa gatatccacc	480	
aggctctgtg aatagggtgg gagctataga gtcctgctgc tggcctcctg cttcctcctg	540	
ggtgggcttt ctccctcagt tagactccat taggggtttg gacagttcct tcctgatctc	600	
ccactcagaa cttcaactac cagtcccaa gctatgtggg cctatattgc atggtgccaa	660	
tggtggctgt acttataaa	679	

<210> 6  
 <211> 80  
 <212> DNA  
 <213> homo sapiens

<400> 6  
 aggggctgga ggttggggac tataaatgcc agaaccttcc attggaccc tc catctttgc 60  
 ctgcaggcag tggcccaagc 80

<210> 7  
 <211> 20  
 <212> DNA  
 <213> homo sapiens

<400> 7  
 tcgtttctat ttccgtggct 20

<210> 8  
 <211> 20  
 <212> DNA  
 <213> homo sapiens

<400> 8  
 cgggagatgg tgtcaattct 20

<210> 9  
 <211> 993  
 <212> DNA  
 <213> homo sapiens

<400> 9  
 atgacaactc ttgttctgc aaccctctcc ttcccttcttc tctggaccct gccaggcag 60  
 gtcctcctca gggtggcctt ggcaaaagag gaagtcaa at ctggAACAA ggggtcccag 120  
 cccatgtccc cctctgattt cctagacaaa cttatggggc gaacatctgg atatgatgcc 180  
 aggattcggc ccaattttaa aggcccaccc gtgaacgtga cctgcaacat cttcatcaac 240  
 agtttcagct ccatcaccaa gaccacaatg gcttgctggg cccctggaa tggcaatgtt 300  
 tctgaaggc ccatatctgc accctcccag gactaccggg tgaatgtctt cttgcggcaa 360  
 cagtggaatg acccacgcct gtcctaccga gaatatcctg atgactctct ggacctcgat 420  
 ccctccatgc tggactctat ctggaaGCCa gacctttctt ttgctaatga gaaaggggcc 480  
 aacttccatg aggtgaccac ggacaacaag ttactgcgc tcttcaagaa tggaaatgtg 540  
 ctgtacagca tcaggctgac cctcattttg tcctgcctga tggacccaa gaacttcccc 600  
 atggacatcc agacctgcac gatgcagctt gagagcttg gctacaccat gaaagacctc 660

gtgtttgagt ggctggaaga tgctcctgct gtccaagtgg ctgaggggct gactctgccc	720
cagtttatct tgccggatga gaaggatcta ggctgttgta ccaagcacta caacacaggg	780
aaattcacct gcatcgaggt aaagttcac ctggAACGGC agatgggcta ctatctgatt	840
cagatgtaca tccccagcct actcatcgtc atcctgtcct gggtctcctt ctggatcaac	900
atggatgctg cccctgcccgt tgtgggcctg ggcacatcacca ccgtgctcac catgaccacc	960
cagagctctg gctccccggc ctctttgcct aag	993

<210> 10  
 <211> 449  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Met Tyr Ser Phe Asn Thr Leu Arg Leu Tyr Leu Ser Gly Ala Ile Val  
 1 5 10 15

Phe Phe Ser Leu Ala Ala Ser Lys Glu Ala Glu Ala Ala Arg Ser Ala  
 20 25 30

Thr Lys Pro Met Ser Pro Ser Asp Phe Leu Asp Lys Leu Met Gly Arg  
 35 40 45

Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro Asn Phe Lys Gly Pro Pro  
 50 55 60

Val Asn Val Ser Cys Asn Ile Phe Ile Asn Ser Phe Gly Ser Ile Ala  
 65 70 75 80

Glu Thr Thr Met Asp Tyr Arg Val Asn Ile Phe Leu Arg Gln Gln Trp  
 85 90 95

Asn Asp Pro Arg Leu Ala Tyr Asn Glu Tyr Pro Asp Asp Ser Leu Asp  
 100 105 110

Leu Asp Pro Ser Met Leu Asp Ser Ile Trp Lys Pro Asp Leu Phe Phe  
 115 120 125

Ala Asn Glu Lys Gly Ala His Phe His Glu Ile Thr Thr Asp Asn Lys  
 130 135 140

Leu Leu Arg Ile Ser Arg Asn Gly Asn Val Leu Tyr Ser Ile Arg Ile  
 145 150 155 160

Thr Leu Thr Leu Ala Cys Pro Met Asp Leu Lys Asn Phe Pro Met Asp  
 165 170 175

Val Gln Thr Cys Ile Met Gln Leu Glu Ser Phe Gly Tyr Thr Met Asn  
 180 185 190

Asp Leu Ile Phe Glu Trp Gln Glu Gln Gly Ala Val Gln Val Ala Asp  
 195 200 205  
 Gly Leu Thr Leu Pro Gln Phe Ile Leu Lys Glu Glu Lys Asp Leu Arg  
 210 215 220  
 Tyr Cys Thr Lys His Tyr Asn Thr Gly Lys Phe Thr Cys Ile Glu Ala  
 225 230 235 240  
 Arg Phe His Leu Glu Arg Gln Met Gly Tyr Tyr Leu Ile Gln Met Tyr  
 245 250 255  
 Ile Pro Ser Leu Leu Ile Val Ile Leu Ser Trp Ile Ser Phe Trp Ile  
 260 265 270  
 Asn Met Asp Ala Ala Pro Ala Arg Val Gly Leu Gly Ile Thr Thr Val  
 275 280 285  
 Leu Thr Met Thr Thr Gln Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys  
 290 295 300  
 Val Ser Tyr Val Lys Ala Ile Asp Ile Trp Met Ala Val Cys Leu Leu  
 305 310 315 320  
 Phe Val Phe Ser Ala Leu Leu Glu Tyr Ala Ala Val Asn Phe Val Ser  
 325 330 335  
 Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg Lys Arg Arg His His  
 340 345 350  
 Lys Glu Asp Glu Ala Gly Glu Gly Arg Phe Asn Phe Ser Ala Tyr Gly  
 355 360 365  
 Met Gly Pro Ala Cys Leu Gln Ala Lys Asp Gly Ile Ser Val Lys Gly  
 370 375 380  
 Ala Asn Asn Ser Asn Thr Thr Asn Pro Pro Pro Ala Pro Ser Lys Ser  
 385 390 395 400  
 Pro Glu Glu Met Arg Lys Leu Phe Ile Gln Arg Ala Lys Lys Ile Asp  
 405 410 415  
 Lys Ile Ser Arg Ile Gly Phe Pro Met Ala Phe Leu Ile Phe Asn Met  
 420 425 430  
 Phe Tyr Trp Ile Ile Tyr Lys Ile Val Arg Arg Glu Asp Val His Asn  
 435 440 445

Gln

<210> 11  
 <211> 465  
 <212> PRT  
 <213> Homo sapiens  
 <400> 11

Met Ala His Val Arg His Phe Arg Thr Leu Val Ser Gly Phe Tyr Phe  
 1 5 10 15

Trp Glu Ala Ala Leu Leu Ser Leu Val Ala Thr Lys Glu Thr Asp  
 20 25 30

Ser Ala Arg Ser Arg Ser Ala Pro Met Ser Pro Ser Asp Phe Leu Asp  
 35 40 45

Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro Asn  
 50 55 60

Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn Ser  
 65 70 75 80

Phe Gly Ser Ile Ala Glu Thr Thr Met Asp Tyr Arg Val Asn Ile Phe  
 85 90 95

Leu Arg Gln Lys Trp Asn Asp Pro Arg Leu Ala Tyr Ser Glu Tyr Pro  
 100 105 110

Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp Lys  
 115 120 125

Pro Asp Leu Phe Phe Ala Asn Glu Lys Gly Ala Asn Phe His Glu Val  
 130 135 140

Thr Thr Asp Asn Lys Leu Leu Arg Ile Phe Lys Asn Gly Asn Val Leu  
 145 150 155 160

Tyr Ser Ile Arg Leu Thr Leu Ser Cys Pro Met Asp Leu Lys  
 165 170 175

Asn Phe Pro Met Asp Val Gln Thr Cys Ile Met Gln Leu Glu Ser Phe  
 180 185 190

Gly Tyr Thr Met Asn Asp Leu Ile Phe Glu Trp Gln Asp Glu Ala Pro  
 195 200 205

Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Leu Leu Lys Glu  
 210 215 220

Glu Lys Asp Leu Arg Tyr Cys Thr Lys His Tyr Asn Thr Gly Lys Phe  
 225 230 235 240

Thr Cys Ile Glu Val Arg Phe His Leu Glu Arg Gln Met Gly Tyr Tyr  
 245 250 255

Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu Ser Trp  
 260 265 270

Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val Ala Leu  
 275 280 285

Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly Ser Arg  
 290 295 300

Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile Trp Met  
 305 310 315 320

Ala Val Cys Leu Leu Phe Val Phe Ser Ala Leu Leu Glu Tyr Ala Ala  
 325 330 335

Val Asn Phe Val Ser Arg Gln His Lys Glu Leu Leu Arg Phe Arg Arg  
 340 345 350

Lys Arg Lys Asn Lys Thr Glu Ala Phe Ala Leu Glu Lys Phe Tyr Arg  
 355 360 365

Phe Ser Asp Met Asp Asp Glu Val Arg Glu Ser Arg Phe Ser Phe Thr  
 370 375 380

Ala Tyr Gly Met Gly Pro Cys Leu Gln Ala Lys Asp Gly Met Thr Pro  
 385 390 395 400

Lys Gly Pro Asn His Pro Val Gln Val Met Pro Lys Ser Pro Asp Glu  
 405 410 415

Met Arg Lys Val Phe Ile Asp Arg Ala Lys Lys Ile Asp Thr Ile Ser  
 420 425 430

Arg Ala Cys Phe Pro Leu Ala Phe Leu Ile Phe Asn Ile Phe Tyr Trp  
 435 440 445

Val Ile Tyr Lys Ile Leu Arg His Glu Asp Ile His His Gln Gln Gln  
 450 455 460

Asp  
 465

<210> 12  
 <211> 337  
 <212> PRT  
 <213> *Mus musculus*

<220>  
 <221> UNSURE  
 <222> (322)..(322)  
 <223> wherein "X" is any amino acid.

<400> 12

Val Ala Leu Ala Lys Glu Asp Val Lys Ser Gly Leu Lys Gly Ser Gln  
 1 5 10 15

Pro Met Ser Pro Ser Asp Phe Leu Asp Lys Leu Met Gly Arg Thr Ser  
 20 25 30

Gly Tyr Asp Ala Arg Ile Arg Pro Asn Phe Lys Gly Pro Pro Val Asn  
 35 40 45

Val Thr Cys Asn Ile Phe Ile Asn Ser Phe Gly Ser Val Thr Glu Thr

50	55	60	
Thr Met Asp Tyr Arg Val Asn Val Phe Leu Arg Gln Gln Trp Asn Asp			
65	70	75	80
Pro Arg Leu Ala Tyr Arg Glu Tyr Pro Asp Asp Ser Leu Asp Leu Asp			
85	90	95	
Pro Ser Met Leu Asp Ser Ile Trp Lys Pro Asp Leu Phe Phe Ala Asn			
100	105	110	
Glu Lys Gly Ala Asn Phe His Glu Val Thr Thr Asp Asn Lys Leu Leu			
115	120	125	
Arg Ile Phe Lys Asn Gly Asn Val Leu Tyr Ser Ile Arg Leu Thr Leu			
130	135	140	
Ile Leu Ser Cys Pro Met Asp Leu Lys Asn Phe Pro Met Asp Ile Gln			
145	150	155	160
Thr Cys Thr Met Gln Leu Glu Ser Phe Gly Tyr Thr Met Asn Asp Leu			
165	170	175	
Met Phe Glu Trp Leu Glu Asp Ala Pro Ala Val Gln Val Ala Glu Gly			
180	185	190	
Leu Thr Leu Pro Gln Phe Ile Leu Arg Asp Glu Lys Asp Leu Gly Tyr			
195	200	205	
Cys Thr Lys His Tyr Asn Thr Gly Lys Phe Thr Cys Ile Glu Val Lys			
210	215	220	
Phe His Leu Glu Arg Gln Met Gly Tyr Tyr Leu Ile Gln Met Tyr Ile			
225	230	235	240
Pro Ser Leu Leu Ile Val Ile Leu Ser Trp Val Ser Phe Trp Ile Asn			
245	250	255	
Met Asp Ala Ala Pro Ala Arg Val Gly Leu Gly Ile Thr Thr Val Leu			
260	265	270	
Thr Met Thr Thr Gln Ser Ser Gly Ser Arg Ala Ser Leu Pro Lys Val			
275	280	285	
Ser Tyr Val Lys Ala Ile Asp Ile Trp Met Ala Val Cys Leu Leu Phe			
290	295	300	
Val Phe Ala Ala Leu Leu Glu Tyr Ala Ala Val Asn Phe Val Ser Arg			
305	310	315	320
Gln Xaa Lys Glu Phe Met Arg Leu Arg Arg Arg Gln Arg Arg Gln Arg			
325	330	335	
Met			

<211> 452  
 <212> PRT  
 <213> Homo sapiens

<400> 13

Met Asn Arg Gln Leu Val Asn Ile Leu Thr Ala Leu Phe Ala Phe Phe  
 1 5 10 15

Leu Glu Thr Asn His Phe Arg Thr Ala Phe Cys Lys Asp His Asp Ser  
 20 25 30

Arg Ser Gly Lys Gln Pro Ser Gln Thr Leu Ser Pro Ser Asp Phe Leu  
 35 40 45

Asp Lys Leu Met Gly Arg Thr Ser Gly Tyr Asp Ala Arg Ile Arg Pro  
 50 55 60

Asn Phe Lys Gly Pro Pro Val Asn Val Thr Cys Asn Ile Phe Ile Asn  
 65 70 75 80

Ser Phe Gly Ser Val Thr Glu Thr Thr Met Asp Tyr Arg Val Asn Ile  
 85 90 95

Phe Leu Arg Gln Gln Trp Asn Asp Ser Arg Leu Ala Tyr Ser Glu Tyr  
 100 105 110

Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met Leu Asp Ser Ile Trp  
 115 120 125

Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Gly Ala Asn Phe His Asp  
 130 135 140

Val Thr Thr Asp Asn Lys Leu Leu Arg Ile Ser Lys Asn Gly Lys Val  
 145 150 155 160

Leu Tyr Ser Ile Arg Leu Thr Leu Thr Leu Ser Cys Pro Met Asp Leu  
 165 170 175

Lys Asn Phe Pro Met Asp Val Gln Thr Cys Thr Met Gln Leu Glu Ser  
 180 185 190

Phe Gly Tyr Thr Met Asn Asp Leu Ile Phe Glu Trp Leu Ser Asp Gly  
 195 200 205

Pro Val Gln Val Ala Glu Gly Leu Thr Leu Pro Gln Phe Ile Leu Lys  
 210 215 220

Glu Glu Lys Glu Leu Gly Tyr Cys Thr Lys His Tyr Asn Thr Gly Lys  
 225 230 235 240

Phe Thr Cys Ile Glu Val Lys Phe His Leu Glu Arg Gln Met Gly Tyr  
 245 250 255

Tyr Leu Ile Gln Met Tyr Ile Pro Ser Leu Leu Ile Val Ile Leu Ser  
 260 265 270

Trp Val Ser Phe Trp Ile Asn Met Asp Ala Ala Pro Ala Arg Val Ala  
 275 280 285

Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Gln Ser Ser Gly Ser  
 290 295 300

Arg Ala Ser Leu Pro Lys Val Ser Tyr Val Lys Ala Ile Asp Ile Trp  
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Original (for SUBMISSION) - printed on 12.02.2002 02:11:41 PM

0-1	Form - PCT/RO/134 (EASY) Indications Relating to Deposited Microorganism(s) or Other Biological Material (PCT Rule 13bis) Prepared using	PCT-EASY Version 2.92 (updated 01.01.2002)
0-2	International Application No.	
0-3	Applicant's or agent's file reference	D0079

1	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
1-1	page	3
1-2	line	20-21
1-3	Identification of Deposit	
1-3-1	Name of depositary institution	American Type Culture Collection
1-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209 United States of America
1-3-3	Date of deposit	24 January 2001 (24.01.2001)
1-3-4	Accession Number	ATCC PTA-2966
1-4	Additional Indications	NONE
1-5	Designated States for Which Indications are Made	all designated States
1-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE

## FOR RECEIVING OFFICE USE ONLY

0-4	This form was received with the international application: (yes or no)	Enclosed <i>Mr</i>
0-4-1	Authorized officer	PCT Operations - LAPD Team 1 367 (703) 915-8700

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0-5	This form was received by the international Bureau on:	07 MAY 2002 (07.05.02)
0-5-1	Authorized officer	

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Organization  
International Bureau



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PCT

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C12N 15/00,

(74) Agents: D'AMICO, Stephen et al.; Bristol-Myers Squibb Company, P.O. Box 4000, Route 206 and Provinceline Road, Princeton, NJ 08543-4000 (US).

(21) International Application Number:

PCT/US2002/004329

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

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Published:

- with international search report
- with (an) indication(s) in relation to deposited biological material furnished under Rule 13bis separately from the description

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1 April 2004

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

WO 2002/066606 A3

(54) Title: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT EXPRESSED IN THE GASTROINTESTINAL TRACT, HGRA4, AND SPLICE VARIANT THEREOF

(57) Abstract: The present invention provides novel polynucleotides encoding HGRA4 polypeptides, fragments and homologues thereof. The present invention also provides novel polynucleotides encoding a HGRA4 splice variant, HGRA4sv. Also provided are vectors, host cells, antibodies, and recombinant and synthetic methods for producing said polypeptides. The invention further relates to diagnostic and therapeutic methods for applying these novel HGRA4 and HGRA4sv polypeptides to the diagnosis, treatment, and/or prevention of various diseases and/or disorders related to these polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of the polynucleotides and polypeptides of the present invention.

**INTERNATIONAL SEARCH REPORT**

International application No.

PCT/US02/04329

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) : C12N 15/00, 15/85, 15/86, C07H 21/04; C07K 14/00  
US CL : 435/69.1, 320.1, 252.3, 325, 6; 536/25.3; 530/350

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 320.1, 252.3, 325, 6; 536/25.3; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
STIC (sequences), STN (Medline, Biosis), EAST

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00/58461 A (RAPPOLD-HOERBRAND) 05 October 2000 (05.10.2000), SEQ ID NO: 1 and 2, page 10, the first paragraph, and claims 1, 2, 7-10.	1-6, 8-10 and 18
X	MATZENBACH, B. et al. Structural analysis of mouse glycine receptor alpha subunit genes. J. Biol. Chem., 28 January 1994, Vol. 269, No. 4, pages 2607-26012, especially Figure 3, page 2608, the right column, the second paragraph..	1-6, 10 and 18
X	Grenningloh, G. et al. Alpha subunit variants of the human glycine receptor: primary structures, functional expression and chromosomal localization of the corresponding genes. The EMBO Journal, 1990, Vol. 9, No. 3, pages 771-776.	1-6, 8-10 and 18

<input type="checkbox"/>	Further documents are listed in the continuation of Box C.	<input type="checkbox"/>	See patent family annex.
*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier application or patent published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search  08 June 2003 (08.06.2003)	Date of mailing of the international search report  05 DEC 2003
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Yvonne Eyler Telephone No. 703-308-0196

**INTERNATIONAL SEARCH REPORT**

International application No.

PCT/US02/04329

**Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3.  Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1.  As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-6, 8-10 and 14-18 directed to SEQ ID NO:3 and 4

**Remark on Protest**  

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

**BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING**

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-6, 8-10 and 14-18, drawn to an isolated nucleic acid, a polypeptide encoded thereby, a vector containing same, a host cell thereof, and a method of recombinantly producing the encoded polypeptide.

Group II, claim(s) 7, drawn to an isolated antibody.

Group III, claim(s) 11 in part, and 19, drawn to a method for treating a medical condition with said polypeptide.

Group IV, claim(s) 11 in part, and 19, drawn to a method for treating a medical condition with said polynucleotide.

Group V, claim(s) 12, drawn to a method of diagnosis by detecting a mutation in said polynucleotide.

Group VI, claim(s) 13, drawn to a method of diagnosis by determining the expression of said polypeptide.

The inventions listed as Groups I-VI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

This authority considers that the main invention in the instant application comprises the first-recited product, an isolated nucleic acid encoding a polypeptide, an expression vector and a host cell containing the nucleic acid; and the first-recited method of using that product, namely a process of recombinant expression and purification of the encoded polypeptide. Note that there is no method of making the nucleic acid. Also included in this group is the product made, namely the encoded polypeptide. The materially and functionally dissimilar products of group II does not share a special technical feature within the meaning of PCT Rule 13.2, and thus do not relate to a single invention concept within the meaning of PCT Rule 13.1. Further, Groups III-VI are directed to various methods, which are designed for different purposes, use different compounds or reagents, involve different method steps, and produce different products and/or different results, which are not coextensive and do not share the same technical feature within the meaning of PCT Rule 13.2 so as to form a single general inventive concept.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

Species 1: SEQ ID NO:3 and 4.

Species 2: SEQ ID NO:74.

Species 3: SEQ ID NO:1 and 2.

The claims are deemed to correspond to the species listed above in the following manner:

Claims 1-19: species 1.

Claims 14-18: species 3.

Claims 5-10 and 13: species 2.

The following claim(s) are generic: none.

The species listed above do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons:

**INTERNATIONAL SEARCH REPORT**

PCT/US02/04329

Species 1-3 are directed to different nucleic acids and polypeptides encoded thereby. Each SEQ ID NO set forth above has distinct chemical, and structural properties, and therefore, each does not share a special technical feature with the other within the meaning of PCT Rule 13.2, and thus do not relate to a single invention concept within the meaning of PCT Rule 13.1.

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